

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:59 ; Search time 9.5 Seconds
(without alignments)
7.985 Million cell updates/sec

Title: 09937009-B
Sequence: 1 fpqfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/prodata/1/pubppa/US09_NEW_PUB pep: *
2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB pep: *
3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB pep: *
4: /EMC_Celerra_SIDS3/prodata/1/pubppa/US08_NEW_PUB pep: *
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6: /EMC_Celerra_SIDS3/prodata/1/pubppa/US10_NEW_PUB pep: *
7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB pep: *
8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	480	US-10-511-814-6	Sequence 6, Appli
2	28	80.0	15	US-11-118-524-4	Sequence 4, Appli
3	28	80.0	109	US-11-293-697-2693	Sequence 2693, Ap
4	28	80.0	147	US-10-953-349-5010	Sequence 5010, Ap
5	28	80.0	170	US-10-953-349-26194	Sequence 26194, A
6	28	80.0	181	US-10-953-349-5009	Sequence 5009, Ap
7	28	80.0	185	US-10-953-349-26193	Sequence 26193, A
8	28	80.0	203	US-10-953-349-5008	Sequence 5008, Ap
9	28	80.0	247	US-10-953-349-27950	Sequence 27950, A
10	28	80.0	334	US-10-953-349-30809	Sequence 30809, A
11	28	80.0	336	US-10-953-349-35132	Sequence 35132, A
12	28	80.0	370	US-10-953-349-30808	Sequence 30808, A
13	28	80.0	376	US-10-953-349-35131	Sequence 35131, A
14	28	80.0	585	US-10-953-349-7243	Sequence 7243, Ap
15	28	80.0	590	US-10-953-349-7242	Sequence 7242, Ap
16	28	80.0	593	US-10-953-349-7241	Sequence 7241, Ap
17	28	80.0	705	US-11-242-317-43	Sequence 43, Appli
18	28	80.0	4373	US-11-118-524-2	Sequence 2, Appli
19	27	77.1	264	US-10-953-349-22672	Sequence 22672, A
20	27	77.1	302	US-10-953-349-22671	Sequence 22671, A
21	27	77.1	328	US-10-953-349-18719	Sequence 18719, A
22	27	77.1	322	US-10-953-349-18839	Sequence 18839, A
23	27	77.1	337	US-10-953-349-22670	Sequence 22670, A
24	27	77.1	356	US-10-953-349-18838	Sequence 18838, A
25	27	77.1	369	US-10-953-349-18837	Sequence 18837, A

26	27	77.1	390	US-10-953-349-18718	Sequence 18718, A
27	27	77.1	395	US-10-953-349-18717	Sequence 18717, A
28	27	77.1	916	US-10-196-749-78	Sequence 78, Appli
29	26	74.3	36	US-10-953-349-15240	Sequence 15240, A
30	26	74.3	145	US-10-953-349-29947	Sequence 29947, A
31	26	74.3	181	US-10-953-349-29946	Sequence 29946, A
32	26	74.3	192	US-10-953-349-19801	Sequence 19801, A
33	26	74.3	194	US-10-953-349-19805	Sequence 19805, Ap
34	26	74.3	201	US-11-293-697-3199	Sequence 3199, Ap
35	26	74.3	246	US-10-953-349-28145	Sequence 28145, A
36	26	74.3	281	US-10-953-349-33611	Sequence 33611, A
37	26	74.3	283	US-10-953-349-33610	Sequence 33610, A
38	26	74.3	286	US-10-953-349-31389	Sequence 31389, A
39	26	74.3	288	US-10-953-349-7304	Sequence 7304, Ap
40	26	74.3	299	US-10-953-349-28144	Sequence 28144, A
41	26	74.3	314	US-10-953-349-5664	Sequence 5664, Ap
42	26	74.3	315	US-10-953-349-5663	Sequence 5663, Ap
43	26	74.3	325	US-10-953-349-23130	Sequence 23130, A
44	26	74.3	339	US-10-953-349-33609	Sequence 33609, A
45	26	74.3	340	US-10-953-349-31388	Sequence 31388, A

ALIGNMENTS

RESULT 1
US-10-511-814-6
; Sequence 6, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2
; CURRENT APPLICATION NUMBER: US/10/511.814
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12567
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-6
Query Match 100.0%; Score 35; DB 6; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FPQFSY 6
Db 469 FPQFSY 474
RESULT 2
US-11-118-524-4
; Sequence 4, Application US/11118524
; Publication No. US20060088847A1
; GENERAL INFORMATION:
; APPLICANT: GU, WEI
; TITLE OF INVENTION: ARF-BP1 AS MEDIATOR OF P53-DEPENDENT AND INDEPENDENT TUMOR
; FILE REFERENCE: 19240-497US2
; CURRENT APPLICATION NUMBER: US/11/118.524
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: 60/610,506
; PRIOR FILING DATE: 2004-09-15

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/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 4
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-118-524-4
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Query Match      80.0%; Score 28; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 PPOFS 5
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Db      8 PPOFS 12
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RESULT 3
US-11-293-697-2693
/ Sequence 2693, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ CURRENT FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2693
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-293-697-2693
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```
Query Match      80.0%; Score 28; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
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Db      61 PPOFS 65
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RESULT 4
US-10-953-349-5010
/ Sequence 5010, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5010
/ LENGTH: 147
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-953-349-5010
```

```
Query Match      80.0%; Score 28; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db      9 PPOFS 13
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```
RESULT 5
US-10-953-349-26194
/ Sequence 26194, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26194
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-953-349-26194
```

```
Query Match      80.0%; Score 28; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db     142 PPOFS 146
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```
RESULT 6
US-10-953-349-5009
/ Sequence 5009, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5009
/ LENGTH: 181
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-953-349-5009
```

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Query Match      80.0%; Score 28; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db      43 PPOFS 47
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```
RESULT 7
US-10-953-349-26193
/ Sequence 26193, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26193
/ LENGTH: 185
/ TYPE: PRT
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ORGANISM: Trilicium aestivum
US-10-953-349-26193

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 185;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 157 PPOFS 161

RESULT 8

US-10-953-349-5008
Sequence 5008, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5008
LENGTH: 203
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-5008

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 203;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 65 PPOFS 69

RESULT 9

US-10-953-349-27950
Sequence 27950, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27950
LENGTH: 247
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-27950

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 247;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPOFS 6
Db 227 PPOFS 232

RESULT 10

US-10-953-349-30809
Sequence 30809, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30809
LENGTH: 334
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-30809

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 334;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 85 PPOFS 89

RESULT 11

US-10-953-349-35132
Sequence 35132, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35132
LENGTH: 336
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-35132

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 336;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 87 PPOFS 91

RESULT 12

US-10-953-349-30808
Sequence 30808, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30808
LENGTH: 370
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-30808

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 370;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
 |||||
 Db 121 PPOFS 125

RESULT 13

US-10-953-349-35131
 ; Sequence 35131, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 35131
 ; LENGTH: 376
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 US-10-953-349-35131

Query Match 80.0%; Score 28; DB 6; Length 376;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
 |||||
 Db 127 PPOFS 131

RESULT 14

US-10-953-349-7243
 ; Sequence 7243, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 7243
 ; LENGTH: 585
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-7243

Query Match 80.0%; Score 28; DB 6; Length 585;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
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 Db 29 PPEFSF 34

RESULT 15

US-10-953-349-7242
 ; Sequence 7242, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 7242
 ; LENGTH: 590
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-7242

Query Match 80.0%; Score 28; DB 6; Length 590;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
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 Db 34 PPEFSF 39

Search completed: June 14, 2006, 02:38:22
 Job time : 10.5 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:09:23 ; Search time 24 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fpqfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	479	1 A59380	protein kinase (EC
2	35	100.0	480	1 A39360	protein kinase (EC
3	35	100.0	480	1 JC2437	protein kinase (EC
4	35	100.0	480	1 S33364	protein kinase (EC
5	35	100.0	480	1 S62117	protein kinase (EC
6	35	100.0	481	1 A46288	protein kinase (EC
7	35	100.0	481	1 JC2438	protein kinase (EC
8	35	100.0	611	1 A55888	protein kinase (EC
9	35	100.0	763	1 A40831	gag-akt polyprotei
10	32	91.4	270	2 T40280	26S proteasome reg
11	32	91.4	655	2 T39064	RNA binding protei
12	31	88.6	241	2 B71128	probable iron (III
13	31	88.6	303	2 H35068	apolipoprotein H-r
14	31	88.6	348	1 MENZFU	matrix protein - S
15	31	88.6	348	1 MENZFU	matrix protein - S
16	31	88.6	348	1 MENZFU	matrix protein - S
17	31	88.6	452	2 A35068	complement factor
18	31	88.6	453	2 T48240	hypothetical prote
19	31	88.6	669	2 AE0919	probable exported
20	31	88.6	682	2 T23813	hypothetical prote
21	31	88.6	808	2 D35069	complement factor
22	31	88.6	1234	1 NBMSH	complement factor
23	30	85.7	241	2 H87684	hypothetical prote
24	30	85.7	302	2 AC3020	GAD65 family prote
25	30	85.7	302	2 F98264	hypothetical prote
26	30	85.7	413	2 G70439	hypothetical prote
27	30	85.7	474	2 T20694	hypothetical prote
28	30	85.7	583	2 T09157	phosphoglucosidase
29	30	85.7	627	2 T02197	hypothetical prote

30	30	85.7	785	2 T11719	probable vacuolar
31	30	85.7	858	2 S50730	hypothetical prote
32	30	85.7	1718	2 T31638	hypothetical prote
33	29	82.9	32	2 S20275	32k protein - Rhod
34	29	82.9	74	2 S16868	gene I3 protein -
35	29	82.9	81	2 S01059	hypothetical prote
36	29	82.9	107	2 G69998	chirodioxin H1 hom
37	29	82.9	151	2 B84751	hypothetical prote
38	29	82.9	169	2 AC0338	probable colicin V
39	29	82.9	332	2 C84061	ferriochrome ABC tr
40	29	82.9	374	2 E83843	hypothetical prote
41	29	82.9	445	2 AE1590	hypothetical prote
42	29	82.9	445	2 AH1649	weakly methyltrans
43	29	82.9	446	2 H95072	hypothetical prote
44	29	82.9	446	2 G97940	hypothetical prote
45	29	82.9	458	2 F97146	probable iron-bull

ALIGNMENTS

RESULT 1
A59380
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C>Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: A59380; A59379
R:Brodebeck, D.; Cron, P.; Hemmings, B.A.
J. Biol. Chem. 274, 9133-9136, 1999
A>Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the activ
A:Reference number: A59380; PMID:99194749; PMID:10092583
A:Accession: A59380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <BRO>
A:Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AAD29089; NID:94757579; PII
R:Masure, S.; Haefner, B.; Weselink, J.J.; Hoefnagel, E.; Mortier, E.; Verhasselt, P.; J
Eur. J. Biochem. 265, 353-360, 1999
A>Title: Molecular cloning, expression and characterization of the human serine/threonine
A:Reference number: A59379; PMID:99421751; PMID:10491192
A:Accession: A59379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <MAS>
A:Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:95804886; PIDN:CAB53537.1
C:Genetics:
A:Gene: GDB:AKT3; PKBG; PRKBG; RAC-gamma
A:Cross-references: GDB:9954867
A:Map position: 1q44-1q44
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein }
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene,
F:7-108/Domain: pleckstrin repeat homology <PLK>
F:149-408/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted
F:305/Binding site: phosphate (Thr) (covalent) #status predicted
F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPQFSY 6
DB 468 FPQFSY 473

RESULT 2
A39360

protein kinase (EC 2.7.1.37) akt1 [validated] - human
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Homo sapiens (man)
 C:Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
 C:Accession: A39360; S36389; S18000; S20836
 R:Jones, P.F.; Jakubowicz, T.; Pitossi, F.U.; Maurer, F.; Hemmings, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
 A:Title: Molecular cloning and identification of a serine/threonine protein kinase of th
 A:Reference number: A39360; PMID:91239529; PMID:1851997
 A:Accession: A39360
 A:Molecule type: mRNA
 A:Residues: 1-480 <ON>
 A:Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E755; GB:M63167; NID:g190827; PIDN:
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A:Reference number: S24423; PMID:92249329; PMID:1533586
 A:Contents: erratum
 A:Accession: S36389
 A:Molecule type: mRNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '
 A:Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA3372.1; PID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinas
 A:Reference number: S17999; PMID:92037600; PMID:1718748
 A:Accession: S18000
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 63-70, 'TPSSSAACSGPLSSNAPMWRLLRSGVDNRHPDGRPPQ', 'EAGGGGDLGVLGTORQLRGRDDGV
 A:Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037
 A:Note: this sequence has been revised in reference S24423
 R:Allesi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
 EMBO J. 15, 6541-6551, 1996
 A:Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
 A:Reference number: A64192; PMID:97133284; PMID:8978661
 A:Contents: annotation; phosphorylation sites
 R:Tooker, A.; Newton, A.C.
 J. Biol. Chem. 275, 8271-8274, 2000
 A:Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD
 A:Reference number: A64193; PMID:20187529; PMID:10722653
 A:Contents: annotation; autophosphorylation site
 C:Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy-1,3
 nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
 C:Genetics:
 A:Gene: GDB:AKT1; RAC; PKB
 A:Cross-references: GDB:118989; OMIM:164730
 A:Map position: 14q32.32-14q32.32
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Pathway: signal transduction pathways regulating various processes including insulin a
 e production
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif
 F:179/Active site: Lys #status predicted
 F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
 F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime

Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPOFSY 6
 Db 469 PPOFSY 474
 RESULT 3
 JC2437
 protein kinase (EC 2.7.1.37) akt1 [validated] - rat
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
 C:Accession: JC2437
 R:Konishi, H.; Shimomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
 Biochem. Biophys. Res. Commun. 205, 817-825, 1994
 A:Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associatio
 A:Reference number: JC2437; PMID:95091823; PMID:7999118
 A:Accession: JC2437
 A:Molecule type: mRNA
 A:Residues: 1-480 <KON>
 A:Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DDBJ:D30040; NID:g485402; PID
 A:Experimental source: testis
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A:Pathway: signal transduction pathways regulating various processes
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif
 F:179/Active site: Lys #status predicted
 F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
 F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
 Query Match 100.0%; Score 35; DB 1; Length 480;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPOFSY 6
 Db 469 PPOFSY 474
 RESULT 4
 S33364
 protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: S33364
 R:Bellacosa, A.; Franke, T.F.; Gonzalez-Porta, M.E.; Datta, K.; Taguchi, T.; Gardner, J.
 Oncogene 8, 745-754, 1993
 A:Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt ar
 A:Reference number: S33364; PMID:93173519; PMID:8437858
 A:Accession: S33364
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-480 <BEL>
 A:Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
 C:Genetics:
 A:Gene: MGI:AKT
 A:Cross-references: MGI:87986
 A:Map position: 12
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A:Pathway: signal transduction pathways regulating various processes
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif

F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 469 PPOFSY 474

RESULT 5

S62117 protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N/Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C/Accession: S62117; S24423; S17999; S15714; S36388
R/Coffier, P.J.; Woodgett, J.R.
Submitted to the EMBL Data Library, December 1991
A/Reference number: S62117
A/Accession: S62117
A/Molecule type: mRNA
A/Residues: 1-480 <COF>

A/Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:9630; PIDN:C
A/Note: This is a revision to the sequence from reference S17999
R/Coffier, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A/Reference number: S24423; MUID:92249329; PMID:1533566
A/Contents: erratum

A/Accession: S24423
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 70-78, 'N', 80-145 <COM>

A/Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
A/Note: this is a revision to the sequence from reference S17999
R/Coffier, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991

A/Title: Molecular cloning and characterization of a novel putative protein-tyrosine kinase
A/Reference number: S17999; MUID:92037600; PMID:1718748
A/Accession: S17999
A/Molecule type: mRNA

A/Residues: 1-70, 'TPSSSAACGPRSSASRTRRSGVDRHHPDGRRAQAGGDDGLPVGJLTRELGGRGNGVAGQAR
A/Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036
A/Note: this sequence has been revised in references S62117 and S24423

C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene

F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 469 PPOFSY 474

RESULT 6

A46288 protein kinase (EC 2.7.1.37) akt2 - human
N/Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
C/Species: Homo sapiens (man)

C/Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004

C/Accession: A46288
R/Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; Thibodeau, N.A.; Acad. Sci. U.S.A. 89, 9267-9271, 1992
A/Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-tyrosine/threonine kinases
A/Reference number: A46288; MUID:93028445; PMID:1409633
A/Accession: A46288
A/Molecule type: mRNA

A/Residues: 1-481 <CHE>
A/Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:9178325; PIDN:J
A/Note: sequence extracted from NCBI backbone (NCBI:P:115859)
C/Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C/Genetics:

A/Gene: GDB:AKT2
A/Cross-references: GDB:135660; OMIM:164731
A/Map position: 19q13.2-19q13.2

C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted

Query Match 100.0%; Score 35; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 470 PPOFSY 475

RESULT 7

JC2438 protein kinase (EC 2.7.1.37) akt2 (validated) - rat
N/Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C/Accession: JC2438

R/Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A/Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A/Reference number: JC2437; MUID:95091823; PMID:7999118
A/Accession: JC2438

A/Molecule type: mRNA
A/Residues: 1-481 <KON>
A/Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:9485404; PIDN:
A/Experimental source: testis
C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes including myoblast
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted

Query Match 100.0%; Score 35; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 470 PPOFSY 475

RESULT 8

A55888 protein kinase (EC 2.7.1.37) akt (similarity) - fruit fly (Drosophila melanogaster)

N/Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase RA
 C/Species: Drosophila melanogaster
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C/Accession: A55888
 R/Andjelkovic, M.; Jones, P.F.; Grosenklau, U.; Cron, P.; Schier, A.F.; Dick, M.; Bilh
 J. Biol. Chem. 270, 4066-4075, 1995
 A/Title: Developmental regulation of expression and activity of multiple forms of the D
 A/Reference number: A55888; MUID:95181376; PMID:7876156
 A/Accession: A55888
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-611 <MND>
 A/Cross-references: UNIPROT:Q24469; UNIPARC:UPI0000866BE; GB:X83510
 C/Genetics:
 A:Gene: FlyBase:RacPK
 A/Cross-references: FlyBase:FBgn013324
 A/Start codon: ACG
 A/Introns: 261/3; 327/3; 457/3; 535/3; 584/3
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A/pathway: signal transduction pathways regulating various processes
 C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threoni
 F/105-209/Domain: pleckstrin repeat homology <PLK>
 F/264-523/Domain: protein kinase homology <KIN>
 F/272-280/Region: protein kinase ATP-binding motif
 F/295/Active site: Lys #status predicted
 F/423/Binding site: phosphate (Thr) (covalent) #status predicted
 F/86/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match

Best Local Similarity 100.0%; Score 35; DB 1; Length 611;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
 |||||

Db 582 FPOFSY 587

RESULT 9

A40831
 gag-akt polypeptide - AKT8 murine leukemia virus
 N/Contents: amino end of core protein p10; core protein p15; inner coat protein p12; kin
 C/Species: AKT8 murine leukemia virus
 C/Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
 C/Accession: A40831; B40831
 R/Bellacosa, A.; Teeter, J.R.; Staal, S.P.; Tischlis, P.N.
 Science 254, 274-277, 1991
 A/Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH
 A/Reference number: A40831; MUID:92022574; PMID:1833819
 A/Accession: A40831
 A/Molecule type: DNA
 A/Residues: 1-262 <BEL>
 A/Cross-references: UNIPARC:UPI00001725AF; GB:M80675
 A/Accession: B40831
 A/Molecule type: DNA
 A/Residues: 262-763 <BE2>
 A/Cross-references: UNIPARC:UPI00001725B0; GB:M80675
 C/Genetics:
 A:Gene: gag-akt
 C/Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase
 F/1-129/Product: core protein p15 #status predicted <CP1>
 F/130-214/Product: inner coat protein p12 #status predicted <CP2>
 F/284-763/Product: kinase-related transforming protein akt #status predicted <AKT>
 F/287-389/Domain: pleckstrin repeat homology <PLK>
 F/431-691/Domain: protein kinase homology <KIN>
 F/439-447/Region: protein kinase ATP-binding motif
 F/25,337/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/462/Active site: Lys #status predicted
 F/609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 763;
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPOFSY 6
 |||||
 Db 752 FPOFSY 757

RESULT 10

T40280
 26S proteasome regulatory complex chain mts3 [validated] - fission yeast (Schizosaccharon
 N/Alternate names: 26S proteasome regulatory complex chain p31 homolog
 C/Species: Schizosaccharomyces pombe
 C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
 C/Accession: T40280; T39593; T52531
 R/McDougal, R.; Rajandream, M.A.; Barrell, B.G.; Saunders, D.; Quail, M.; Harris, D.
 submitted to the EMBL Data Library, July 1999
 A/Reference number: Z21917
 A/Accession: T40280
 A/Molecule type: DNA
 A/Residues: 1-159 <MCD>
 A/Cross-references: UNIPROT:P50524; UNIPARC:UPI000016210B; EMBL:AL096809; PIDN:CA846777.1
 R/Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
 submitted to the EMBL Data Library, May 1998
 A/Reference number: Z21866
 A/Accession: T39593
 A/Molecule type: DNA
 A/Residues: 127-270 <LYN>
 A/Cross-references: UNIPARC:UPI0000169070; EMBL:AL023554; PIDN:CAA19021.1; GSPDB:GN00067;
 R/Gordon, C.; McGurk, G.; Wallace, M.; Hastie, N.D.
 J. Biol. Chem. 271, 5704-5711, 1996
 A/Title: A conditional lethal mutation in the fission yeast 26S protease subunit mts3+ is c
 A/Reference number: Z26102
 A/Accession: T52531
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-270 <GOR>
 A/Cross-references: UNIPARC:UPI000012F86D; EMBL:X92682; PIDN:CAA63366.1
 C/Genetics:
 A:Gene: mts3
 C/Function:
 A/Description: responsible for transition from metaphase to anaphase [validated, MUID:96;
 C/Superfamily: human 26S proteasome regulatory complex chain p31
 C/Keywords: proteasome; protein degradation

Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 270;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
 |||||

Db 157 FPEFSY 162

RESULT 11

T39064
 RNA binding protein - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T39064
 R/Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, V.
 submitted to the EMBL Data Library, August 1997
 A/Reference number: Z21825
 A/Accession: T39064
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-655 <MUR>
 A/Cross-references: UNIPROT:Q92347; UNIPARC:UPI000013A99A; EMBL:Z81317; PIDN:CAB03604.1;
 A/Experimental source: strain 972h-; cosmid c6G9
 C/Genetics:
 A:Gene: SPDB:SPAC6G9.02C
 A/Map position: 1

Query Match 91.4%; Score 32; DB 2; Length 655;

Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 246 FPOFAY 251

RESULT 12

B71128
probable iron (III) dicitrate transport ATP-binding protein - *Pyrococcus horikoshii*
C/Species: *Pyrococcus horikoshii*
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C/Accession: B71128
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Onitoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: B71128
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-241 <XAM>
A/Cross-references: UNIPROT:O58521; UNIPARC:UPI00006680B; GB:AP000003; NID:G3236130; PI
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by Genbank
A/Genes: PH0791
C/Keywords: ATP
F/21-204/Domain: ATP-binding cassette homology <ABC>

Query Match 88.6%; Score 31; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 88 FPOFSF 93

RESULT 13

H35068
apolipoprotein H-related protein 23L1 - mouse
C/Species: *Mus musculus* (house mouse)
C/Date: 27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: H35068; A35069; B35069; I35068
R/Vlk, D.P.; Munoz-Canoves, P.; Kozono, H.; Martin, L.G.; Tack, B.F.; Chaplin, D.D.
J. Biol. Chem. 265, 3193-3201, 1990
A/Title: Identification and sequence analysis of four complement factor H-related trans
A/Reference number: A35070; MUID:90153965; PMID:1689298
A/Accession: H35068
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-303 <VIK>
A/Cross-references: UNIPROT:O61405; UNIPARC:UPI0000248D8; GB:M29007; NID:G192557; PIDN:
C/Note: translation of the nucleotide sequence is not complete
C/Superfamily: complement C3d/Bpstein-Barr virus receptor; complement factor H repeat ho
C/Keywords: duplication
F/28-81/Domain: complement factor H repeat homology <FH01>
F/86-146/Domain: complement factor H repeat homology <FH02>
F/150-203/Domain: complement factor H repeat homology <FH03>
F/212-266/Domain: complement factor H repeat homology <FH04>

Query Match 88.6%; Score 31; DB 2; Length 303;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 88 FPOFXY 93

RESULT 14

MFNZFU
matrix protein - Sendai virus (strain Fushimi)

C/Species: Sendai virus
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S10330
R/Willembrink, W.; Neubert, W.J.
Nucleic Acids Res. 18, 3993, 1990
A/Title: Cloning and sequencing of the matrix protein gene (M) of Sendai virus (strain F
A/Reference number: S10330; MUID:90326529; PMID:2165255
A/Accession: S10330
A/Molecule type: genomic RNA
A/Residues: 1-348 <WIL>
A/Cross-references: UNIPROT:P17748; UNIPARC:UPI000013897A; GB:X53056; NID:G62017; PIDN:C
A/Experimental source: ATCC VR-105
C/Genetics:
A/Genes: M
C/Keywords: matrix protein

C/Keywords: matrix protein

Query Match 88.6%; Score 31; DB 1; Length 348;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 7 FPKFSY 12

RESULT 15

MFNZS
matrix protein - Sendai virus (strain Harris)

C/Species: Sendai virus
C/Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C/Accession: A04042
R/Blumberg, B.M.; Rose, K.; Simona, M.G.; Roux, L.; Giorgi, C.; Kolakofsky, D.
J. Virol. 52, 656-663, 1984
A/Title: Analysis of the Sendai virus M gene and protein.
A/Reference number: A04042; MUID:85033911; PMID:6092688
A/Accession: A04042
A/Molecule type: genomic RNA
A/Residues: 1-348 <BLU>
A/Cross-references: UNIPROT:P03426; UNIPARC:UPI000013897B; GB:K02742; NID:G334935; PIDN:
C/Superfamily: parainfluenza virus matrix protein

Query Match 88.6%; Score 31; DB 1; Length 348;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 7 FPKFSY 12

Search completed: June 14, 2006, 02:17:20
Job time : 25 secs

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:59 ; Search time 9.5 Seconds
(without alignments)
7.985 Million cell updates/sec

Title: 09937009-A

Perfect score: 36

Sequence: 1 finddy 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*
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3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/prodata/1/pubppa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/prodata/1/pubppa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/prodata/1/pubppa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	33	91.7	463 6 US-10-953-349-2983	Sequence 2983, Ap
2	33	91.7	464 6 US-10-953-349-2982	Sequence 2982, Ap
3	33	91.7	483 6 US-10-953-349-2981	Sequence 2981, Ap
4	32	88.9	163 7 US-11-293-697-2752	Sequence 2752, Ap
5	31	86.1	247 6 US-10-511-937-2422	Sequence 2422, Ap
6	31	86.1	1924 6 US-10-512-386-56	Sequence 56, Appl
7	30	83.3	292 6 US-10-953-349-7286	Sequence 7286, Ap
8	30	83.3	300 6 US-10-953-349-7285	Sequence 7285, Ap
9	30	83.3	402 6 US-10-953-349-7284	Sequence 7284, Ap
10	30	83.3	429 6 US-10-953-349-7283	Sequence 7283, Ap
11	29	80.6	197 6 US-10-953-349-23710	Sequence 23710, A
12	29	80.6	511 7 US-11-316-521-31	Sequence 31, Appl
13	29	80.6	525 7 US-11-313-836-10	Sequence 10, Appl
14	29	80.6	571 6 US-10-953-349-31976	Sequence 31976, A
15	29	80.6	640 6 US-10-953-349-31975	Sequence 31975, A
16	29	80.6	669 6 US-10-953-349-31974	Sequence 31974, A
17	28	77.8	271 6 US-10-953-349-12760	Sequence 12760, A
18	28	77.8	280 7 US-11-293-697-3893	Sequence 3893, Ap
19	28	77.8	485 6 US-10-953-349-12759	Sequence 12759, A
20	28	77.8	4051 6 US-10-501-834-7	Sequence 7, Appl
21	28	77.8	4059 6 US-10-501-834-6	Sequence 6, Appl
22	28	77.8	4074 6 US-10-501-834-2	Sequence 2, Appl
23	27	75.0	118 6 US-10-506-063A-6	Sequence 6, Appl
24	27	75.0	256 6 US-10-953-349-19900	Sequence 19900, A
25	27	75.0	300 6 US-10-953-349-19899	Sequence 19899, A

26	27	75.0	340 6 US-10-953-349-17750	Sequence 17750, A
27	27	75.0	418 6 US-10-953-349-17749	Sequence 17749, A
28	27	75.0	439 6 US-10-953-349-19898	Sequence 19898, A
29	27	75.0	439 7 US-11-181-115-33	Sequence 33, Appl
30	27	75.0	439 7 US-11-181-115-45	Sequence 45, Appl
31	27	75.0	479 6 US-10-953-349-17748	Sequence 17748, A
32	27	75.0	488 7 US-11-317-983-5	Sequence 5, Appl
33	27	75.0	498 7 US-11-317-983-4	Sequence 4, Appl
34	27	75.0	530 6 US-10-471-571A-2082	Sequence 2082, Ap
35	26	72.2	104 6 US-10-953-349-39811	Sequence 39811, A
36	26	72.2	112 6 US-10-953-349-34760	Sequence 34760, A
37	26	72.2	129 6 US-10-370-959-130	Sequence 130, App
38	26	72.2	163 6 US-10-953-349-28654	Sequence 28654, A
39	26	72.2	195 6 US-10-953-349-28653	Sequence 28653, A
40	26	72.2	234 6 US-10-471-571A-3990	Sequence 3990, Ap
41	26	72.2	268 6 US-10-953-349-25610	Sequence 25610, A
42	26	72.2	296 6 US-10-953-349-25609	Sequence 25609, A
43	26	72.2	303 6 US-10-953-349-11752	Sequence 11752, A
44	26	72.2	339 6 US-10-953-349-11751	Sequence 11751, A
45	26	72.2	675 7 US-11-293-697-3326	Sequence 3326, Ap

ALIGNMENTS

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RESULT 1
US-10-953-349-2983
; Sequence 2983, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2983
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2983
; Sequence 2982, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2982
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2982
Query Match 91.7%; Score 33; DB 6; Length 463;
Best Local Similarity 83.3%; Pred. NO. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 320 FKDFDY 325

RESULT 3

US-10-953-349-2981
; Sequence 2281, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2981
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2981

Query Match 91.7%; Score 33; DB 6; Length 483;
Best Local Similarity 83.3%; Pred. No. 9.7;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 339 FKDFDY 344

RESULT 4

US-11-293-697-2752
; Sequence 2752, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2752
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2752

Query Match 88.9%; Score 32; DB 7; Length 163;
Best Local Similarity 83.3%; Pred. No. 4.8;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 149 FRDPDY 154

RESULT 5

US-10-511-937-2422
; Sequence 2422, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2422
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2422

Query Match 86.1%; Score 31; DB 6; Length 247;
Best Local Similarity 83.3%; Pred. No. 12;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 178 FRDPDH 183

RESULT 6

US-10-512-386-56
; Sequence 56, Application US/10512386
; Publication No. US2006008837A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
; FILE REFERENCE: GFU-A0203YIP
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4706
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1924
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-512-386-56

Query Match 86.1%; Score 31; DB 6; Length 1924;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 1500 FEDFDY 1505

RESULT 7

US-10-953-349-7286
; Sequence 7286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7286
LENGTH: 292
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-7286

Query Match 83.3%; Score 30; DB 6; Length 292;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 58 FSDFDY 63

RESULT 8
US-10-953-349-35355
Sequence 35355, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35355
LENGTH: 300
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-35355

Query Match 83.3%; Score 30; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RDPDY 6
Db 218 RDPDY 222

RESULT 9
US-10-953-349-7285
Sequence 7285, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7285
LENGTH: 402
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-7285

Query Match 83.3%; Score 30; DB 6; Length 402;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDFDY 6

Db 168 FSDFDY 173

RESULT 10
US-10-953-349-7284
Sequence 7284, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7284
LENGTH: 429
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-7284

Query Match 83.3%; Score 30; DB 6; Length 429;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 195 FSDFDY 200

RESULT 11
US-10-953-349-23710
Sequence 23710, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23710
LENGTH: 197
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-23710

Query Match 80.6%; Score 29; DB 6; Length 197;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 4 FLDFDY 9

RESULT 12
US-11-316-521-31
Sequence 31, Application US/11316521
Publication No. US20060111848A1
GENERAL INFORMATION:
APPLICANT: Carlrow, Clotilde K.S.
APPLICANT: Foster, Jeremy
APPLICANT: Zhang, Yinhua
APPLICANT: Kumar, Sanjay
TITLE OF INVENTION: Identification and Use of Cofactor Independent Phosphoglycerate
Mutase as a Drug Target for Pathogenic Organisms and Treatment c
TITLE OF INVENTION: the Same
FILE REFERENCE: NEB-230-PCIP-US

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; CURRENT APPLICATION NUMBER: US/11/316,521
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US 60/483,566
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: PCT/US2004/018200
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; US-11-316-521-31
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Query Match      80.6%; Score 29; DB 7; Length 511;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FRDPD 5
Db      277 FRDPD 281
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RESULT 13
; US-11-313-836-10
; Sequence 10, Application US/11313836
; Publication No. US20060116508A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorraine P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SCL, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; FILE REFERENCE: MP103-0620NMIM
; CURRENT APPLICATION NUMBER: US/11/313,836
; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: US/10/426,776
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229,662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795,691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105,992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406,045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314,881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 525
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; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-313-836-10
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Query Match      80.6%; Score 29; DB 7; Length 525;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 FRDPDY 6
Db      150 FRDPDY 155
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RESULT 14
; US-10-953-349-31976
; Sequence 31976, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31976
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31976
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Query Match      80.6%; Score 29; DB 6; Length 571;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 FRDPDY 6
Db      287 FRDPDY 292
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RESULT 15
; US-10-953-349-31975
; Sequence 31975, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31975
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31975
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Query Match      80.6%; Score 29; DB 6; Length 640;
Best Local Similarity 83.3%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 FRDPDY 6
Db      356 FRDPDY 361
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Job time : 9.5 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:29 ; Search time 124.5 Seconds
(Without alignments)
22.324 Million cell updates/sec

Title: 09937009-A

Sequence: 1 firstdy 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	36	100.0	6	4	US-10-148-786A-55
2	36	100.0	6	4	US-10-217-574-9
3	36	100.0	6	4	US-10-217-555-8
4	36	100.0	11	4	US-10-217-574-25
5	36	100.0	11	4	US-10-217-555-25
6	36	100.0	11	4	US-10-217-574-4
7	36	100.0	23	4	US-10-148-786A-5
8	36	100.0	23	4	US-10-217-574-23
9	36	100.0	23	4	US-10-217-555-23
10	36	100.0	24	4	US-10-148-786A-22
11	36	100.0	24	4	US-10-217-574-12
12	36	100.0	24	4	US-10-217-555-11
13	36	100.0	35	4	US-10-380-235-33
14	36	100.0	35	4	US-10-380-235-35
15	36	100.0	39	4	US-10-148-786A-3
16	36	100.0	39	4	US-10-148-786A-14
17	36	100.0	39	5	US-10-994-093-13
18	36	100.0	39	5	US-10-922-337-9
19	36	100.0	39	6	US-11-192-341-3
20	36	100.0	77	4	US-10-148-786A-8
21	36	100.0	334	4	US-10-217-574-18
22	36	100.0	334	4	US-10-217-555-18
23	36	100.0	725	5	US-10-491-467-45
24	36	100.0	786	3	US-09-950-041-2
25	36	100.0	786	3	US-10-732-563-2
26	36	100.0	786	4	US-10-732-796A-2
27	36	100.0	786	5	US-10-491-997-50

28	36	100.0	786	5	US-10-975-909-2	Sequence 2, Appl1
29	36	100.0	984	4	US-10-029-905-10	Sequence 10, Appl
30	36	100.0	984	4	US-10-354-358-106	Sequence 106, App
31	33	91.7	224	3	US-09-882-227-100	Sequence 100, App
32	33	91.7	235	4	US-10-335-977-5500	Sequence 5500, Ap
33	33	91.7	236	4	US-10-335-977-5501	Sequence 5501, Ap
34	33	91.7	329	5	US-10-501-282-5990	Sequence 5990, Ap
35	33	91.7	352	6	US-11-097-143-9603	Sequence 9603, Ap
36	33	91.7	464	5	US-10-739-930-5983	Sequence 5983, Ap
37	33	91.7	940	4	US-10-437-963-106389	Sequence 106389, Ap
38	33	91.7	1390	4	US-10-039-112-2	Sequence 2, Appl1
39	33	91.7	1390	5	US-10-761-983-2	Sequence 2, Appl1
40	33	91.7	2237	6	US-11-010-775-15	Sequence 15, Appl
41	32	88.9	158	4	US-10-424-599-27452	Sequence 27452, Ap
42	32	88.9	163	4	US-10-108-260A-2752	Sequence 2752, Ap
43	32	88.9	169	3	US-09-764-875-691	Sequence 691, App
44	32	88.9	175	3	US-09-764-881-144	Sequence 144, App
45	32	88.9	175	3	US-09-764-881-144	Sequence 144, App

ALIGNMENTS

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RESULT 1
US-10-148-786A-55
; Sequence 55, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148.786A
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-786A-55

Query Match      100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FRDPDY 6
Db 1 FRDPDY 6

RESULT 2
US-10-217-574-9
; Sequence 9, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217.574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
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/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-574-9
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Query Match          100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY          1 FRDPDY 6
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Db          1 FRDPDY 6
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RESULT 3
US-10-217-555-8
/ Sequence 8, Application US/10217555
/ Publication No. US2004009569A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
/ FILE REFERENCE: 44236
/ CURRENT APPLICATION NUMBER: US/10/217,555
/ CURRENT FILING DATE: 2002-12-05
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-555-8
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Query Match          100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY          1 FRDPDY 6
            |||||
Db          1 FRDPDY 6
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```
RESULT 4
US-10-217-574-25
/ Sequence 25, Application US/10217574
/ Publication No. US2004005687A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures
/ FILE REFERENCE: 44237
/ CURRENT APPLICATION NUMBER: US/10/217,574
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: GB 0216215.4
/ PRIOR FILING DATE: 2002-07-12
/ NUMBER OF SEQ ID NOS: 46
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/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-574-25
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Query Match          100.0%; Score 36; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY          1 FRDPDY 6
            |||||
Db          2 FRDPDY 7
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RESULT 5
US-10-217-555-25
/ Sequence 25, Application US/10217555
/ Publication No. US2004009569A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
/ FILE REFERENCE: 44236
/ CURRENT APPLICATION NUMBER: US/10/217,555
/ CURRENT FILING DATE: 2002-12-05
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-555-25
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Query Match          100.0%; Score 36; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY          1 FRDPDY 6
            |||||
Db          2 FRDPDY 7
```

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RESULT 6
US-10-217-574-4
/ Sequence 4, Application US/10217574
/ Publication No. US2004005687A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures
/ FILE REFERENCE: 44237
/ CURRENT APPLICATION NUMBER: US/10/217,574
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: GB 0216215.4
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;; PRIOR FILING DATE: 2002-07-12
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C-terminal
;; OTHER INFORMATION: tail
US-10-217-574-4

Query Match 100.0%; Score 36; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 6 FRDPDY 11

RESULT 7
US-10-148-786A-5
; Sequence 5, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-5

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 13 FRDPDY 18

RESULT 8
US-10-217-574-23
; Sequence 23, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-574-23

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 9
US-10-217-555-23
; Sequence 23, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-555-23

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 10
US-10-148-786A-22
; Sequence 22, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-10-148-786A-22

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Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 11
US-10-217-574-12
; Sequence 12, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:

; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-574-12

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 12
US-10-217-555-11
; Sequence 11, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:

; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-555-11

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 13
US-10-380-235-33
; Sequence 33, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:

; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,423
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/238,558
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-235-33

Query Match 100.0%; Score 36; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 29 FRDPDY 34

RESULT 14
US-10-380-235-35
; Sequence 35, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:

; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: 60/237,423
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/238,558
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 35
 ; LENGTH: 35
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-380-235-35

Query Match 100.0%; Score 36; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
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 Db 29 FRDFDY 34

RESULT 15
 US-10-148-786A-3
 ; Sequence 3, Application US/10148786A
 ; Publication No. US20030143656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aleasi, Dario
 ; APPLICANT: Biondi, Riccardo
 ; TITLE OF INVENTION: Protein Kinase Regulation
 ; FILE REFERENCE: 002.00210
 ; CURRENT APPLICATION NUMBER: US/10/148,786A
 ; CURRENT FILING DATE: 2003-01-08
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 3
 ; LENGTH: 39
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
 US-10-148-786A-3

Query Match 100.0%; Score 36; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
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 Db 29 FRDFDY 34

Search completed: June 14, 2006, 02:37:57
 Job time : 125.5 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model1

Run on: June 14, 2006, 02:16:55 ; Search time 38 Seconds
(without alignments)
13.821 Million cell updates/sec

Title: 09937009-A
Perfect score: 36
Sequence: 1 frdfdy 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	36	100.0	672	2 US-09-949-002-522	Sequence 522, App
2	36	100.0	786	2 US-09-949-002-351	Sequence 351, App
3	36	100.0	1041	2 US-09-949-016-7878	Sequence 7878, App
4	33	91.7	176	2 US-09-248-796A-18362	Sequence 18362, A
5	33	91.7	209	2 US-09-270-767-41925	Sequence 41925, A
6	33	91.7	993	2 US-08-836-687B-30	Sequence 30, Appl
7	33	91.7	1390	2 US-08-770-544-2	Sequence 2, Appl
8	33	91.7	1390	2 US-09-579-259-2	Sequence 2, Appl
9	33	91.7	1390	2 US-09-650-324A-2	Sequence 2, Appl
10	33	91.7	1390	2 US-10-039-112A-2	Sequence 2, Appl
11	32	88.9	114	2 US-09-513-999C-7038	Sequence 7038, App
12	32	88.9	345	2 US-09-248-796A-20158	Sequence 20158, A
13	31	86.1	226	1 US-07-929-198-2	Sequence 2, Appl
14	31	86.1	226	1 US-07-929-198-4	Sequence 4, Appl
15	31	86.1	226	1 US-07-929-198-6	Sequence 6, Appl
16	31	86.1	226	1 US-08-557-146-15	Sequence 15, Appl
17	31	86.1	226	1 US-09-154-344-15	Sequence 15, Appl
18	31	86.1	226	1 US-08-944-483-43	Sequence 43, Appl
19	31	86.1	1924	2 US-09-866-557A-2	Sequence 2, Appl
20	30	83.3	118	2 US-09-254-180C-3	Sequence 3, Appl
21	30	83.3	118	2 US-09-065-059-5	Sequence 5, Appl
22	30	83.3	118	2 US-08-913-555-5	Sequence 5, Appl
23	30	83.3	119	2 US-09-254-180C-16	Sequence 16, Appl
24	30	83.3	119	2 US-09-254-180C-18	Sequence 18, Appl
25	30	83.3	119	2 US-09-254-180C-19	Sequence 19, Appl
26	30	83.3	119	2 US-09-254-180C-149	Sequence 149, App

27	30	83.3	119	2 US-08-913-555-23	Sequence 23, Appl
28	30	83.3	138	2 US-09-254-180C-143	Sequence 143, App
29	30	83.3	219	2 US-09-254-180C-180	Sequence 180, App
30	30	83.3	281	2 US-09-605-703B-114	Sequence 114, App
31	30	83.3	281	2 US-09-605-703B-116	Sequence 116, App
32	30	83.3	718	2 US-09-252-991A-28229	Sequence 28229, A
33	30	83.3	789	2 US-09-712-363-244	Sequence 244, App
34	29	80.6	85	2 US-09-621-976-4345	Sequence 4345, App
35	29	80.6	124	2 US-09-270-767-33226	Sequence 33226, A
36	29	80.6	124	2 US-09-270-767-48443	Sequence 48443, A
37	29	80.6	136	2 US-09-270-767-32985	Sequence 32985, A
38	29	80.6	136	2 US-09-270-767-48202	Sequence 48202, A
39	29	80.6	147	2 US-09-270-767-31908	Sequence 31908, A
40	29	80.6	147	2 US-09-270-767-33287	Sequence 33287, A
41	29	80.6	147	2 US-09-270-767-47125	Sequence 47125, A
42	29	80.6	147	2 US-09-270-767-48504	Sequence 48504, A
43	29	80.6	148	2 US-09-640-211A-787	Sequence 787, App
44	29	80.6	151	2 US-09-270-767-32172	Sequence 32172, A
45	29	80.6	151	2 US-09-270-767-33218	Sequence 33218, A

ALIGNMENTS

```

RESULT 1
US-09-949-002-522
Sequence 522, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 522
LENGTH: 672
TYPE: PRT
ORGANISM: Human
US-09-949-002-522

Query Match      100.0%; Score 36; DB 2; Length 672;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FRDPDY 6
Db      175 FRDPDY 180

RESULT 2
US-09-949-002-351
Sequence 351, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 351
LENGTH: 786

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TYPE: PRT
ORGANISM: Human
US-09-949-002-351

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 786;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 3
US-09-949-016-7878
Sequence 7878, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7878

LENGTH: 1041

TYPE: PRT

ORGANISM: Human

US-09-949-016-7878

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 1041;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 1031 FRDPDY 1036

RESULT 4
US-09-248-796A-18362
Sequence 18362, Application US/09248796A
Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18362

LENGTH: 176

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-18362

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 176;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 97 FRDPDY 102

RESULT 5
US-09-270-767-41925
Sequence 41925, Application US/09270767
Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

PRIOR FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 41925

LENGTH: 209

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-41925

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 209;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 128 FRDPDY 133

RESULT 6
US-08-836-687B-30
Sequence 30, Application US/08836687B
Patent No. 6448034

GENERAL INFORMATION:
APPLICANT: Gasson, Michael John

TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN

FILE REFERENCE: 20747/70

CURRENT APPLICATION NUMBER: US/08/836,687B

PRIOR FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 993

TYPE: PRT

ORGANISM: Lactococcus sp.

US-08-836-687B-30

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 993;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 595 YRDPDY 600

RESULT 7
US-08-770-544-2
Sequence 2, Application US/08770544
Patent No. 5907085

GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis

TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND

THEIR USES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1390 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-770-544-2

Query Match 91.7%; Score 33; DB 1; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
:|||||
Db 421 YRDPDY 426

RESULT 8
US-09-579-259-2
Sequence 2, Application US/09579259
Patent No. 6558953
GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
LING, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/579,259
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1390 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-579-259-2

Query Match 91.7%; Score 33; DB 2; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
:|||||
Db 421 YRDPDY 426

RESULT 9
US-09-650-324A-2
Sequence 2, Application US/09650324A
Patent No. 6638720
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
LING, KAI-SHU
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
THEIR USES
FILE REFERENCE: 07678/025006
CURRENT APPLICATION NUMBER: US/09/650,324A
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR FILING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 08/770,544
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: US 60/009,008
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1390
TYPE: PRT
ORGANISM: Grapevine leafroll virus
US-09-650-324A-2

Query Match 91.7%; Score 33; DB 2; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
:|||||
Db 421 YRDPDY 426

RESULT 10
US-10-039-112A-2
Sequence 2, Application US/10039112A
Patent No. 6916617
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
LING, KAI-SHU
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
THEIR USES
FILE REFERENCE: 07678/025007
CURRENT APPLICATION NUMBER: US/10/039,112A
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 09/650,324

PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR FILING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 08/770,544
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: US 60/009,008
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 1390
TYPE: PR
ORGANISM: Grapevine leafroll virus
US-10-039-112A-2

Query Match 91.7%; Score 33; DB 2; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 421 YRDPDY 426

RESULT 11
US-09-513-999C-7038
Sequence 7038, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7038
LENGTH: 114
TYPE: PR
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: UNSURE
LOCATION: 103
OTHER INFORMATION: Xaa=Glu or Gly
US-09-513-999C-7038

Query Match 88.9%; Score 32; DB 2; Length 114;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 13 FRDPDY 18

RESULT 12
US-09-248-796A-20158
Sequence 20158, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20158
LENGTH: 345
TYPE: PR
ORGANISM: Candida albicans
US-09-248-796A-20158

Query Match 88.9%; Score 32; DB 2; Length 345;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 7 FRDPDY 12

RESULT 13
US-07-929-198-2
Sequence 2, Application US/07929198
Patent No. 5567602
GENERAL INFORMATION:
APPLICANT: Clark, James M.
APPLICANT: Shoemaker, Kevin R.
APPLICANT: Warne, Robert L.
TITLE OF INVENTION: Recombinant Production of Chymase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,198
FILING DATE: 19920812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7056-017-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-929-198-2

Query Match 86.1%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 157 FRDPDY 162

RESULT 14
US-07-929-198-4

Sequence 4, Application US/07929198
Patent No. 5567602
GENERAL INFORMATION:
APPLICANT: Clark, James M.
APPLICANT: Shoemaker, Kevin R.
APPLICANT: Warne, Robert L.
TITLE OF INVENTION: Recombinant Production of Chymase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,198
FILING DATE: 19920812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7056-017-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-929-198-4

Query Match 86.1%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 157 FRDPDH 162

RESULT 15
US-07-929-198-6
Sequence 6, Application US/07929198
Patent No. 5567602
GENERAL INFORMATION:
APPLICANT: Clark, James M.
APPLICANT: Shoemaker, Kevin R.
APPLICANT: Warne, Robert L.
TITLE OF INVENTION: Recombinant Production of Chymase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,198

FILING DATE: 19920812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7056-017-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-929-198-6

Query Match 86.1%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 157 FRDPDH 162

Search completed: June 14, 2006, 02:18:39
Job time : 39 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:38 ; Search time 154.5 Seconds
(without alignments)
17.756 Million cell updates/sec

Title: 00937009-A
Perfect score: 36
Sequence: 1 fcdidy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	36	100.0	6	ABR57448	Abi57448 PKB activ
2	36	100.0	6	ADJ38853	Adj38853 PKR2 AGC
3	36	100.0	11	ABR57456	Abi57456 Protein k
4	36	100.0	11	ADB92666	Adb92666 Peptide p
5	36	100.0	11	ADV91663	Adv91663 Activated
6	36	100.0	15	ADB92676	Adb92676 Crystall
7	36	100.0	23	ABR98805	Abbr98805 3-phospho
8	36	100.0	23	ABR57454	Abi57454 Protein k
9	36	100.0	23	ADB92664	Adb92664 Peptide p
10	36	100.0	23	ADV91662	Adv91662 Activated
11	36	100.0	24	AAV94729	Aay94729 Region B
12	36	100.0	24	AAV94726	Aay94726 Peptide c
13	36	100.0	24	ABR99799	Abbr99799 Protein k
14	36	100.0	24	ABR99794	Abbr99794 3-phospho
15	36	100.0	24	ABR57451	Abi57451 PKB activ
16	36	100.0	25	ADY20891	Ady20891 PDK1-inte
17	36	100.0	35	AAE22774	Aae22774 Human SGK
18	36	100.0	39	ABR98812	Abbr98812 PDK1 pept
19	36	100.0	39	ABR98806	Abbr98806 3-phospho
20	36	100.0	39	ADJ38899	Adj38899 PDK1tide
21	36	100.0	39	ADQ43310	Adq43310 Human PDK
22	36	100.0	39	ADR23147	Adr23147 Human sub
23	36	100.0	39	ADT07106	Adt07106 3'-phosph

24	36	100.0	39	ADV67122	Adv67122 3'-phosph
25	36	100.0	39	ADW86518	Adw86518 Substrate
26	36	100.0	39	ADZ87403	Adz87403 PKRtide p
27	36	100.0	39	ABR17979	Abi17979 Peptide u
28	36	100.0	39	ABR97117	Abi97117 Human kin
29	36	100.0	39	AEF68515	Aef68515 3-phospho
30	36	100.0	77	ABR9793	Abbr9793 3-phospho
31	36	100.0	91	ADY20895	Ady20895 PDK-1 inh
32	36	100.0	91	ADY20892	Ady20892 PDK-1 inh
33	36	100.0	315	ABR99835	Abbr99835 AGC prote
34	36	100.0	315	ADJ38883	Adj38883 PKR2 amin
35	36	100.0	334	ABR57466	Abi57466 AGC fam11
36	36	100.0	343	ADY20896	Ady20896 PDK-1 inh
37	36	100.0	345	ADY20894	Ady20894 GFP-conju
38	36	100.0	385	ABR98822	Abbr98822 AGC prote
39	36	100.0	725	ADC99092	Adc99092 Human KPP
40	36	100.0	786	AAW86349	Aaw86349 Human DNA
41	36	100.0	786	AAE16090	Aae16090 Human DNA
42	36	100.0	786	ADC78821	Adc78821 Human PRO
43	36	100.0	786	ADE25535	Ade25535 Human rel
44	36	100.0	786	ADP56650	Adp56650 Human Tol
45	36	100.0	786	ADP48591	Adp48591 Human Tol

ALIGNMENTS

RESULT 1
ID ABR57448 standard; peptide; 6 AA.
XX ABR57448;
DT 15-SEP-2003 (first entry)
XX
DE PKB activity modulating peptide #12.
XX
KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
KW protein co-ordinate data; cytosolic; antidiabetic; vasodilator; PKB;
KW neurotrophic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
KW structural analysis; cancer; diabetes; erectile dysfunction;
KW neurodegeneration.
XX
OS Synthetic.
XX
XX WO2003016516-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-GB003735.
XX
XX 14-AUG-2001; 2001GB-00019860.
XX
XX 01-MAY-2002; 2002GB-00009985.
XX
PA (NOVS) NOVARTIS FORSCHUNGSSITFTUNG ZWEIGNIEDERL.
XX (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD;
XX WPI; 2003-268328/26.
XX
XX New crystal of protein kinase B beta, useful for activating protein
XX PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
XX PT or a tetragonal space group.
XX
XX Claim 32; Page 265; 284pp; English.
XX
XX The present invention describes a crystal of protein kinase B beta
XX (PKBbeta) comprising (II) where (II) comprises: (a) a tetragonal space
XX group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
XX 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
XX minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
XX plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =

CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
 CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
 CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
 CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
 CC the specification. (1) has cytosolic, antidiabetic, vasotropic,
 CC neurotropic and neuroprotective activities, and can be used in gene
 CC therapy. The crystal of PKBbeta, and methods from the present invention,
 CC are useful in activating protein kinases, particularly AGC kinases, for
 CC identifying modulators of protein kinase activity, and for structural
 CC analysis of other protein kinases. The crystal may also be used in
 CC manufacturing a medicament for treating cancers, diabetes, erectile
 CC dysfunction or neurodegeneration. The present sequence represents a
 CC peptide which can be used in a method from the present invention to
 CC modulate PKB activity

SO Sequence 6 AA;

Query Match 100.0%; Score 36; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
 Db 1 FRDPDY 6

RESULT 2
 ADJ38853
 ID ADJ38853 standard; peptide; 6 AA.

XX ADJ38853;
 XX 06-MAY-2004 (first entry)
 XX PRK2 AGC hydrophobic motif peptide.

DE phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;
 XX protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 XX insulin signalling pathway; signalling; crystalline form;
 XX protein co-ordinate data; three-dimensional structure; antifungal;
 XX antidiabetic; cardiant; cytosolic; cerebroprotective; vasotropic;
 XX anorectic; protein kinase modulator; cancer; diabetes; obesity;
 XX apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 XX neural injury.

OS Synthetic.
 XX WO2003104481-A2.
 XX 18-DEC-2003.
 XX 09-JUN-2003; 2003WO-GB002509.
 XX 08-JUN-2002; 2002GB-00013185.
 XX (UYDU-) UNITV DUNDEE.
 XX Alessei D, Biondi R, Komander D, Van AD;
 XX WPI; 2004-062373/06.
 XX Selecting/designing compound for modulating activity of phosphoinositide
 XX dependent protein kinase 1 by using molecular modelling to select/design
 XX compound predicted to interact with protein kinase catalytic domain.
 XX Disclosure; Page 17; 383pp; English.

CC The present invention describes a method (M1) for selecting or designing
 CC a compound for modulating the activity of phosphoinositide dependent
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to
 CC select or design a compound that is predicted to interact with the
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is
 CC predicted to interact with the protein kinase catalytic domain. Also

CC described: (1) selecting or designing (M2) a compound for modulating the
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 CC kinase having a hydrophobic pocket in the position equivalent to the
 CC hydrophobic pocket of human PDK1 that is defined by residues including
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
 CC PDK1 and further having a phosphate binding pocket in the position
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined
 CC by residues including Lys76, Arg131, Thr148 and/or Glu150. (2) assessing
 CC (M3) the activation state of a structure for a protein kinase: (3) a
 CC mutated protein kinase (1); (4) a polynucleotide (11) encoding (1); (5) a
 CC host cell (111) comprising (11); (6) identifying (M4) a compound that
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 CC (7) an antibody (1V) reactive with the phosphate binding pocket of PDK1
 CC or (1) or an antibody reactive with PDK1 or (1) but not with the protein
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a
 CC compound (V) identified or identifiable by (M1) or (M2); (9) use of (V),
 CC (1), (11) in medicine; (10) use of (V), (1), (11) for the manufacture of
 CC a medicament for the treatment of a patient in need of modulation of
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 CC p70 S6 kinase, for example insulin signalling pathway and/or
 CC PDK1/PDK2/SGK/PKB/p70 S6 kinase/PKC signalling; and (11) a
 CC crystalline form (VI) of polypeptide as defined in (M1). (1) has
 CC antifungal, antidiabetic, cardiant, cytosolic, cerebroprotective,
 CC vasotropic and anorectic activities, and can be used as a modulator of
 CC protein kinase. (V) is useful for modulating the ability of protein
 CC kinase to phosphorylate different substrates, e.g., different naturally
 CC occurring polypeptides, to different extents. (V) inhibits or increases
 CC the activity of protein kinase. The protein structures e.g., the co-
 CC ordinates as provided in the specification are useful for designing
 CC reagent useful in drug designing assays or characterisation of protein
 CC kinase activity or regulation. (V) capable of producing the activity of
 CC PKC, e.g., PKC beta, PRK1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.

SO Sequence 6 AA;

Query Match 100.0%; Score 36; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
 Db 1 FRDPDY 6

RESULT 3
 ABR57456
 ID ABR57456 standard; peptide; 11 AA.

XX ABR57456;
 XX 15-SEP-2003 (first entry)
 XX Protein kinase B assay related peptide PIFtide1.

DE Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
 XX protein co-ordinate data; cytosolic; antidiabetic; vasotropic; PKB;
 XX neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
 XX structural analysis; cancer; diabetes; erectile dysfunction;
 XX neurodegeneration.

OS Synthetic.
 XX WO2003016516-A2.
 XX 27-FEB-2003.

PF 14-AUG-2002; 2002MO-GB003735.
XX
XX 14-AUG-2001; 2001GB-00019860.
PR 01-MAY-2002; 2002GB-00009985.
XX
XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD;
PI WPI; 2003-268329/26.
XX
XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX Disclosure; Page 86; 284pp; English.
XX
XX The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space
CC group P4₁-2₁-1₂ and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (II) has cytoskeletal, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which is used in the exemplification of the present invention
XX
SQ Sequence 11 AA;
XX
Query Match 100.0%; Score 36; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 2 FRDPDY 7
XX
RESULT 4
ADB92666
ID ADB92666 standard; peptide; 11 AA.
XX
XX ADB92666;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX Peptide PIFcidel.
DE
XX
XX Protein kinase Bbeta; PKBbeta; cytoskeletal; antidiabetic; vasotropic;
KW neurotropic; neuroprotective; gene therapy; cancer; diabetes;
KW erectile dysfunction; neurodegeneration; protein co-ordinate data;
KW enzyme; AGC kinase.
XX
XX Synthetic.
OS
XX
XX MO2003016517-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002MO-GB003737.
PF
XX
XX 14-AUG-2001; 2001GB-00019860.
PR

PR 01-MAY-2002; 2002GB-00009985.
PR 12-JUL-2002; 2002GB-00016215.
XX
XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD;
PI WPI; 2003-268329/26.
XX
XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX Disclosure; Page 104; 124pp; English.
XX
XX The invention relates to a crystal of protein kinase Bbeta (PKBbeta).
CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancers, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents a peptide used in a
CC protein kinase B assay.
XX
SQ Sequence 11 AA;
XX
Query Match 100.0%; Score 36; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 2 FRDPDY 7
XX
RESULT 5
ADV91663
ID ADV91663 standard; peptide; 11 AA.
XX
XX ADV91663;
AC
XX
XX 24-FEB-2005 (first entry)
DT
XX
XX Activated protein kinase B beta (PKBbeta) peptide, PIFcidel #2.
DE
XX
XX Pharmaceutical; cell signaling; chemotherapy; AGC kinase related disease;
KW cancer; diabetes; neurodegenerative disease; Alzheimers disease;
KW Parkinsons disease; AIDS associated dementia;
KW amyotrophic lateral sclerosis; multiple sclerosis; schizophrenia;
KW scleroderma; cardiomyocyte hypertrophy; reperfusion; ischemia; baldness;
KW neuroprotective; antiparkinsonian; neurotropic; anti-hiv; neuroleptic;
KW cardiovascular-gen.; endocrine-gen.; vasotropic; cytoskeletal;
KW antidiabetic; protein kinase B beta; PKBbeta.
XX
XX Unidentified.
OS
XX
XX EP1466488-A1.
PN
XX
XX 15-DEC-2004.
PD
XX
XX 10-JUN-2003; 2003EP-00090177.
PF
XX
XX 10-JUN-2003; 2003EP-00090177.
PR
XX
XX (PHOS-) PHOSPHOSITES GMBH.
PA
XX
XX Blondi R, Engel M;
PI

XX WPI; 2005-041631/05.
DR
XX
XX New kecone, amide, ester and carbonyl derivatives useful for treating
PT e.g. cancer, multiple sclerosis, amyotrophic lateral sclerosis, and
PT Alzheimer's disease, Parkinson's disease, reperfusion, ischemia and
PT diabetes.
XX
XX Disclosure; Page 3; 32pp; English.
PS
XX
CC The present invention relates to small molecules that are protein kinase
CC regulators, activators and inhibitors, compositions containing such
CC compounds and their pharmaceutical use. The invention is useful for the
CC prevention or treatment of a disease related to an AGC kinase such as
CC cancer, diabetes, neurodegenerative diseases, Alzheimer's disease,
CC Parkinson's disease, AIDS associated dementia, amyotrophic lateral
CC sclerosis, multiple sclerosis, schizophrenia, cardiomyocyte hypertrophy,
CC reperfusion, ischemia and baldness. The present sequence is an activated
CC protein kinase B beta (PKBbeta) peptide, Pfifide. PKB belong to the AGC
CC kinase group of enzymes.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 36; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
|||
Db 2 FRDFDY 7

RESULT 6
ADB92676
ID ADB92676 standard; peptide; 15 AA.

XX ADB92676;

AC 01-JAN-2004 (first entry)

XX Crystallised PKBbeta molecule C-terminal tail.

XX Protein kinase Bbeta; PKBbeta; cytostatic; antidiabetic; vasotropic;
KM nootropic; neuroprotective; gene therapy; cancer; diabetes;
KM erectile dysfunction; neurodegeneration; protein co-ordinate data;
KW enzyme; AGC kinase.

XX Unidentified.

OS WO2003016517-A2.

XX 27-FEB-2003.

PD 14-AUG-2002; 2002WO-GB003737.

XX 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-0000985.

PR 12-JUL-2002; 2002GB-00016215.

XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.

PA (CANC-) CANCER RES INST.

XX Barford D, Yang J, Hemmings BA, Cron PD;

XX WPI; 2003-268329/26.

XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.

XX Claim 6; Page 232; 124pp; English.

XX The invention relates to a crystal of protein kinase Bbeta (PKBbeta).

CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancers, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents the crystallised
CC PKBbeta molecule C-terminal tail.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
|||
Db 6 FRDFDY 11

RESULT 7
AAB99805
ID AAB99805 standard; peptide; 23 AA.

XX AAB99805;

AC 20-SEP-2001 (first entry)

XX 3-phosphoinositide-dependent protein kinase 1 interacting peptide #2.

XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;
KM diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.

XX Homo sapiens.

OS Synthetic.

XX WO200144497-A2.

XX 21-JUN-2001.

PD 04-DEC-2000; 2000WO-GB004598.

XX 02-DEC-1999; 99US-0168559P.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R;

XX WPI; 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides.

XX Claim 14; Page 130; 180pp; English.

XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of a
CC hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
CC polynucleotides from the present invention are useful in medicine,
CC particularly in the manufacture of a medicament for treating a patient in
CC need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is in

CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischemic injury, including stroke. The compound or composition
CC is also useful for inhibiting the degree or rate of phosphorylation by
CC the protein kinase. The interacting polypeptide or compound is useful in
CC methods of stabilizing a hydrophobic pocket-containing protein kinase,
CC where the protein kinase is exposed to the compound or polypeptide.
CC AAB9786 to AAB9847 represent amino acid sequences, and AAH4210 and
CC AAH4211 represent oligonucleotide sequences, used in the exemplification
CC of the present invention

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 13 FRDPDY 18

RESULT 8
ABR57454
ID ABR57454 standard; peptide; 23 AA.

XX ABR57454;

DT 15-SEP-2003 (first entry)

DE Protein kinase B assay related peptide Pifitide.

XX Protein kinase B: PKB/Akt; enzyme; crystal structure; drug discovery;
KW protein co-ordinate data; cyrostatic; antidiabetic; vasotropic; PKB;
KW neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
KW structural analysis; cancer; diabetes; erectile dysfunction;
KW neurodegeneration.

XX Synthetic.

OS WO2003016516-A2.

XX PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-GB003735.

PR 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-00009985.

XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.

PI Barford D, Yang J, Hemmings BA, Cron PD;

XX WPI; 2003-268328/26.

PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.

XX Disclosure; Page 86; 284pp; English.

CC The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (1), where (1) comprises: (a) a tetragonal space
CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cyrostatic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene

CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancer, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which is used in the exemplification of the present invention

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 36; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 14 FRDPDY 19

RESULT 9
ADB92664
ID ADB92664 standard; peptide; 23 AA.

XX ADB92664;

DT 01-JAN-2004 (first entry)

DE Peptide Pifitide.

XX Protein kinase Bbeta; PKBbeta; cyrostatic; antidiabetic; vasotropic;
KW neurotropic; neuroprotective; gene therapy; cancer; diabetes;
KW erectile dysfunction; neurodegeneration; protein co-ordinate data;
KW enzyme; AGC kinase.

XX Synthetic.

OS WO2003016517-A2.

XX PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-GB003737.

PR 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-00009985.

PR 12-JUL-2002; 2002GB-00016215.

XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.

PI Barford D, Yang J, Hemmings BA, Cron PD;

XX WPI; 2003-268329/26.

PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.

XX Disclosure; Page 104; 124pp; English.

CC The invention relates to a crystal of protein kinase Bbeta (PKBbeta).
CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancer, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents a peptide used in a
CC protein kinase B assay.

SQ Sequence 23 AA;
Query Match 100.0%; Score 36; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDFDY 6
14 FRDFDY 19
Db 14 FRDFDY 19
RESULT 10
ADV91662
ID ADV91662 standard; peptide; 23 AA.
AC ADV91662;
XX 24-FEB-2005 (first entry)
DE Activated protein kinase B beta (PKBbeta) peptide, Piflide #1.
XX Pharmacological; cell signaling; chemotherapy; AGC kinase related disease;
KW cancer; diabetes; neurodegenerative disease; Alzheimers disease;
KW Parkinsons disease; AIDS associated dementia;
KW amyotrophic lateral sclerosis; multiple sclerosis; schizophrenia;
KW scleroderma; cardiomyocyte hypertrophy; reperfusion; ischemia; baldness;
KW neuroprotective; antiparkinsonian; nootropic; anti-hiv; neuroleptic;
KW cardiovascular-gen.; endocrine-gen.; vasotropic; cyostatic;
KM antidiabetic; protein kinase B beta; PKBbeta.
XX
XX Unidentified.
XX
XX EPI486488-A1.
XX
XX 15-DEC-2004.
PD 10-JUN-2003; 2003EP-00090177.
XX
XX 10-JUN-2003; 2003EP-00090177.
PR 10-JUN-2003; 2003EP-00090177.
XX
PA (PHOS-) PHOSPHOSITES GMBH.
XX
PI Biondi R, Engel M;
XX
XX WPI; 2005-041631/05.
DR
XX New ketone, amide, ester and carbonyl derivatives useful for treating
PT e.g. cancer, multiple sclerosis, amyotrophic lateral sclerosis,
PT Alzheimer's disease, Parkinson's disease, reperfusion, ischemia and
PT diabetes.
XX
XX Disclosure; Page 3; 32pp; English.
XX
XX The present invention relates to small molecules that are protein kinase
CC regulators, activators and inhibitors, compositions containing such
CC compounds and their pharmaceutical use. The invention is useful for the
CC prevention or treatment of a disease related to an AGC kinase such as
CC cancer, diabetes, neurodegenerative diseases, Alzheimer's disease,
CC Parkinson's disease, AIDS associated dementia, amyotrophic lateral
CC sclerosis, multiple sclerosis, schizophrenia, cardiomyocyte hypertrophy,
CC reperfusion, ischemia and baldness. The present sequence is an activated
CC protein kinase B beta (PKBbeta) peptide, Piflide. PKB belong to the AGC
CC kinase group of enzymes.
XX
SQ Sequence 23 AA;
Query Match 100.0%; Score 36; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDFDY 6
14 FRDFDY 19
Db 14 FRDFDY 19

RESULT 11
AAV94729
ID AAV94729 standard; peptide; 24 AA.
XX
XX AAV94729;
AC
XX
XX 29-JAN-2001 (first entry)
DE
XX Region B of protein kinase C related protein kinase 2.
XX
XX Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
KW protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
KW mechanical tissue damage; ischaemic disease; stroke;
KW myocardial infarction; antigenic peptide.
XX
XX Unidentified.
OS
XX
XX WO200056864-A2.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 17-MAR-2000; 2000WO-GB001004.
PP
XX
XX 19-MAR-1999; 99GB-00006245.
PR
XX
XX (UYDU-) UNIV DUNDEE.
PA
XX
XX Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
PI
XX
XX WPI; 2000-647155/62.
DR
XX
XX
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
PT interacting polypeptide.
XX
XX
XX Disclosure; Page 11; 103pp; English.
PS
XX
XX This invention relates to a method for altering the substrate specificity
CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
CC an interacting polypeptide. Included in the invention are a preparation
CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
CC specificity is useful for phosphorylating a residue corresponding to the
CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
CC -Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
CC protein kinase C related protein kinase 2 (PRK2). The compound identified
CC by methods of the invention that are capable of altering the substrate
CC specificity of PDK1 are useful for manufacturing a medicament for
CC treating a patient who is in need of modulation of the insulin signalling
CC pathway and/or PDK1, PDK2 or PRK2 signalling. A compound that is capable
CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1
CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
CC SGK, may be capable of providing a survival signal that protects cells
CC from apoptosis induced in a variety of ways. Reduction of the activity of
CC PDK1 may promote apoptosis and may be useful in treating cancer.
CC Conditions in which aiding apoptosis may be of benefit may also include
CC resolution of inflammation. A compound capable of increasing the activity
CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
CC levels of leptin, which may lead to weight loss. The compounds may
CC suppress apoptosis, which may aid cell survival during or following cell
CC damaging processes and in treating disease in which apoptosis is
CC involved. Examples of the diseases include, mechanical (including heart)
CC tissue injury or ischaemic disease, for example stroke and myocardial
CC infarction, or neural injury. The present sequence represents a region of
CC protein kinase C related protein kinase 2 (PRK2) which interacts with
CC PDK1
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 36; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDFDY 6
 |||||
 14 FRDFDY 19

Db 14 FRDFDY 19

RESULT 12
 AAY94726
 ID AAY94726 standard; peptide; 24 AA.

XX AAY94726;
 XX
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Peptide capable of altering substrate specificity of PDK1.

KM Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
 KM protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KM mechanical tissue damage; ischaemic disease; stroke;
 KM myocardial infarction; antigenic peptide.

XX
 OS Unidentified.
 XX
 PN WO200056864-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-GB001004.
 XX
 PR 19-MAR-1999; 99GB-00006245.
 XX
 PA (UYDU-) UNIV DUNDEE.

PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 XX
 XX WPI; 2000-647155/62.

PT Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide.
 XX
 PS Disclosure; Page 9; 103pp; English.

XX This invention relates to a method for altering the substrate specificity
 CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
 CC an interacting polypeptide. Included in the invention are a preparation
 CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
 CC specificity is useful for phosphorylating a residue corresponding to the
 CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
 CC Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
 CC protein kinase C related protein kinase 2 (PRK2). The compound identified
 CC by methods of the invention that are capable of altering the substrate
 CC specificity of PDK1 are useful for manufacturing a medicament for
 CC treating a patient who is in need of modulation of the insulin signalling
 CC pathway and/or PDK1. PDK2 or PRK2 signalling. A compound that is capable
 CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1
 CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
 CC SGK, may be capable of providing a survival signal that protects cells
 CC from apoptosis induced in a variety of ways. Reduction of the activity of
 CC PDK1 may promote apoptosis and may be useful in treating cancer.

CC Conditions in which aiding apoptosis may be of benefit may also include
 CC resolution of inflammation. A compound capable of increasing the activity
 CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
 CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
 CC levels of leptin, which may lead to weight loss. The compounds may
 CC suppress apoptosis, which may aid cell survival during or following cell
 CC damaging processes, and in treating disease in which apoptosis is
 CC involved. Examples of the diseases include, mechanical (including heart)
 CC tissue injury or ischaemic disease, for example stroke and myocardial
 CC infarction, or neural injury. The present sequence represents a potential
 CC PDK1 substrate peptide. The peptide is capable of altering the substrate
 CC specificity of PDK1 in the method of the invention

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 36; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDFDY 6
 |||||
 14 FRDFDY 19

Db 14 FRDFDY 19

RESULT 13
 AAB99799
 ID AAB99799 standard; peptide; 24 AA.

XX AAB99799;
 XX
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Protein kinase derived interacting peptide #1.

KM Protein kinase; identification; hydrophobic pocket; interacting; cancer;
 KM diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.

XX
 OS Homo sapiens.
 XX
 PN WO200144497-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 04-DEC-2000; 2000WO-GB004598.
 XX
 PR 02-DEC-1999; 99US-0168559P.
 XX
 PA (UYDU-) UNIV DUNDEE.

PI Alessi D, Biondi R;
 XX
 XX WPI; 2001-390252/41.

PT Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides.
 XX
 PS Disclosure; Page 25; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of a
 CC hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
 CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
 CC polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient in
 CC need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is in
 CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or composition
 CC is also useful for inhibiting the degree or rate of phosphorylation by
 CC the protein kinase. The interacting polypeptide or compound is useful in
 CC methods of stabilising a hydrophobic pocket-containing protein kinase,
 CC where the protein kinase is exposed to the compound or polypeptide.
 CC AAB99786 to AAB99847 represent amino acid sequences, and AAB44210 and
 CC AAB44211 represent oligonucleotide sequences, used in the exemplification
 CC of the present invention

XX Sequence 24 AA;
 SQ

```
Query Match      100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 FRDPDY 6
      |||||
Db      14 FRDPDY 19

RESULT 14
AAB9794
ID AAB9794 standard; peptide; 24 AA.
AC AAB9794;
XX
XX
DT 20-SEP-2001 (first entry)
DE 3-phosphoinositide-dependent protein kinase 1 binding peptide PIFide.
XX
XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;
KM diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200144497-A2.
XX
XX 21-JUN-2001.
XX
XX 04-DEC-2000; 2000WO-GB004598.
XX
XX 02-DEC-1999; 99US-0168559P.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Aleesi D, Biondi R;
XX
XX WPI; 2001-390252/41.
XX
XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides.
XX
XX Disclosure; Page 22; 180pp; English.
XX
XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of a
CC hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
CC polynucleotides from the present invention are useful in medicine.
CC Particularly in the manufacture of a medicament for treating a patient in
CC need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is in
CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischaemic injury, including stroke. The compound or composition
CC is also useful for inhibiting the degree or rate of phosphorylation by
CC the protein kinase. The interacting polypeptide or compound is useful in
CC methods of stabilising a hydrophobic pocket-containing protein kinase,
CC where the protein kinase is exposed to the compound or polypeptide.
CC AAB9786 to AAB99847 represent amino acid sequences, and AAH44210 and
CC AAH44211 represent oligonucleotide sequences, used in the exemplification
CC of the present invention
XX
XX Sequence 24 AA;
SQ

Query Match      100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 FRDPDY 6
      |||||
Db      14 FRDPDY 19

RESULT 15
ABR57451
ID ABR57451 standard; peptide; 24 AA.
AC ABR57451;
XX
XX
XX 15-SEP-2003 (first entry)
DE PKB activity modulating peptide #15.
XX
XX Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
KM protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;
KM neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
KM structural analysis; cancer; diabetes; erectile dysfunction;
XX neurodegeneration.
XX
XX Synthetic.
XX
XX WO2003016516-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-GB003735.
XX
XX 14-AUG-2001; 2001GB-00019860.
XX
XX 01-MAY-2002; 2002GB-00009985.
XX
XX (NOVS ) NOVARTIS FORSCHUNGSSIFTUNG ZWEIGNIEDERL.
XX (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD,
XX
XX WPI; 2003-268328/26.
XX
XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX Claim 32; Page 265; 284pp; English.
XX
XX The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (1), where (1) comprises: (a) a tetragonal space
CC group P41-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cytostatic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which can be used in a method from the present invention to
CC modulate PKB activity
XX
XX Sequence 24 AA;
SQ

Query Match      100.0%; Score 36; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 FRDPDY 6
|||
Db 14 FRDPDY 19

Search completed: June 14, 2006, 02:09:01
Job time : 157.5 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:58 ; Search time 218 Seconds
(without alignments)
25.459 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fpgfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	27	2	06PWW2_CANFA
2	35	100.0	36	2	09N1C5_BOVIN
3	35	100.0	37	2	09N1C6_SHEEP
4	35	100.0	66	2	06PWW1_CANFA
5	35	100.0	198	2	08C6X4_MOUSE
6	35	100.0	201	2	09BV07_HUMAN
7	35	100.0	246	2	09PUJ3_CHICK
8	35	100.0	256	2	09N582_CABEL
9	35	100.0	302	2	04TBD9_TETNG
10	35	100.0	353	2	08CE74_MOUSE
11	35	100.0	419	2	0519W5_CANFA
12	35	100.0	472	2	04SLA7_TETNG
13	35	100.0	478	2	0802Y3_BRARE
14	35	100.0	478	1	AKT3_HUMAN
15	35	100.0	479	1	AKT3_MOUSE
16	35	100.0	479	2	05VTI1_HUMAN
17	35	100.0	479	2	06NWX0_MOUSE
18	35	100.0	480	1	AKT1_BOVIN
19	35	100.0	480	1	AKT1_HUMAN
20	35	100.0	480	1	AKT1_MOUSE
21	35	100.0	480	1	AKT1_RAT
22	35	100.0	480	1	05ER56_BOVIN
23	35	100.0	480	2	06GSA6_MOUSE
24	35	100.0	480	2	057513_CHICK
25	35	100.0	481	1	AKT1_XENLA
26	35	100.0	481	1	AKT2_HUMAN
27	35	100.0	481	1	AKT2_MOUSE
28	35	100.0	481	1	AKT2_RAT
29	35	100.0	481	2	03HSE5_RAT
30	35	100.0	481	2	03TY95_MOUSE
31	35	100.0	485	1	AKT2B_XENLA

32	35	100.0	486	1	AKT2A_XENLA	Q7zx15 xenopus lae
33	35	100.0	501	1	AKT_MLVAR	P31748 akt8 murine
34	35	100.0	523	2	Q4T057_TETNG	P31748 akt8 murine
35	35	100.0	611	1	AKT1_DROME	Q8ind9 drosophila
36	32	91.4	96	2	Q4NMG3_BACCE	Q4mg3 bacillus ce
37	32	91.4	96	2	Q37M0_BACCE	Q637m0 bacillus ce
38	32	91.4	96	2	Q6HFJ2_BACCH	Q6hfj2 bacillus th
39	32	91.4	96	2	Q81Y91_BACAN	Q81y91 bacillus an
40	32	91.4	96	2	Q73JN3_BACCI	Q73jn3 bacillus ce
41	32	91.4	101	2	Q3EDM1_BACTI	Q3edm1 bacillus th
42	32	91.4	101	2	Q812Z5_BACCR	Q812z5 bacillus th
43	32	91.4	160	2	Q3JAI5_NITOC	Q3jai5 nitrosococ
44	32	91.4	175	2	Q36GM8_9GAMM	Q36gm8 shewanella
45	32	91.4	254	2	Q3HG86_TRIIR	Q3hg86 trichodesmi

ALIGNMENTS

RESULT 1
ID 06PWW2_CANFA PRELIMINARY; PRT; 27 AA.
AC 06PWW2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Protein Kinase B gamma-like protein (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mirna Escobar H., Meyer J., Winkler S., Schelling C., Dolf G.,
RA Nolte I., Bullerdiek J.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC EMBL; AY575065; AAS89304.1; ?; Genomic DNA.
DR Ensembl; ENSCAFG0000015806; Canis familiaris.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON TER 1
SQ SEQUENCE 27 AA; 3145 MW; E65A150C3808A39A CRC64;
Query Match 100.0%; Score 35; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPGFSY 6
Db 16 FPGFSY 21
RESULT 2
ID 09N1C5_BOVIN PRELIMINARY; PRT; 36 AA.
AC 09N1C5;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Protein kinase B (Fragment).
GN Name=AKT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RX MEDLINE=20458865; PubMed=11003702; DOI=10.1007/s003350010150;
RA Fahrnkrug S.C., Freking B.A., Rexroad C.E. III, Leymaster K.A.,
RA Kappes S.M., Smith T.P.L.;
RT "Comparative mapping of the ovine clpg locus.";
RL Mamm. Genome 11:871-876(2000).
CC -----
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CC -----
DR EMBL: AF207874; AAF67084.1; -; Genomic DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER
SQ SEQUENCE 36 AA; 4055 MW; EFC17D6728155130 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 25 PPOFSY 30

RESULT 3
ID O9N1C6_SHEEP PRELIMINARY; PRT; 37 AA.
AC O9N1C6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Protein kinase B (Fragment).
GN Name=AKT;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fahrnkrug S.C., Freking B.A., Rexroad C.E. III, Leymaster K.A.,
RA Kappes S.M., Smith T.P.L.;
RT "Comparative mapping of the ovine clpg locus.";
RL Mamm. Genome 0:0-0(2000).
CC -----
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CC -----
DR EMBL: AF207873; AAF67083.1; -; Genomic DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER
SQ SEQUENCE 37 AA; 4115 MW; 9AA56E9B5C894882 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 26 PPOFSY 31

RESULT 4
ID O6PVM1_CANFA PRELIMINARY; PRT; 66 AA.
AC O6PVM1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Protein kinase B gamma-like protein (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Murua Escobar H., Borrmann L., Nimzyk R., Nolte I., Bullerdick J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AY575066; AAS89305.1; -; mRNA.
DR Ensembl: ENSCAFG0000015806; Canis familiaris.
DR GO: GO:005524; F:ATP binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR Pfam: PF00433; Pkinase_C; 1.
DR SMART: SM00133; S_TK_X; 1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 66 AA; 7752 MW; 0A08B63B19BE68C7 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 55 PPOFSY 60

RESULT 5
ID O8C6X4_MOUSE PRELIMINARY; PRT; 198 AA.
AC O8C6X4;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE 15 days embryo head cDNA, RIKEN full-length enriched library,
DE clone: D930002M15 product: thymoma viral proto-oncogene 3, full insert
DE sequence. (Fragment).
GN Name=Akt3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells K., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilm M., Aldred L.G., Ainslie V., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailei A.M.,
RA Bamsel M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christofideis A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Iakeo K., Iwama A., Ishikawa T.,

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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Livovich L., Liu J.,
 RA Luna S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motegut-Tabar S., Mulder N., Nakano N., Nakashiki H., Ng P.,
 RA Nalson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlowski V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Schobach C., Sekiguchi K., Sempke C.A., Seno S., Seesa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tamajo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahstedt C., Matlick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimiyu N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nkaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Braet D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guelinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Namata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haseizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barab G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki K., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hamaguchi T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
 RA Saito R., Saiton H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 EMBL: AK052953; BAC35219.1; -; mRNA.
 HSSP: P31751; 1MRX.
 SRR: O8C6X4; 1-178.
 DR Ensembl; ENSMUSG0000019699; Mus musculus.
 DR MGI; MGI:1345147; Akt3.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00433; Kinase_C; 1.

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
FT NON TER 1
SQ SEQUENCE 198 AA; 22644 MW; 242F9CDD03C7ABE9 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 187 PPOFSY 192

RESULT 6
Q9BV07_HUMAN PRELIMINARY; PRT; 201 AA.
AC Q9BV07;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
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EMBL; BC001737; AAH01737.1; -; mRNA.
DR HSSP; P31751; IMRY.
DR SMR; Q9BV07; 1-183.
DR Ensembl; ENSG00000142208; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:000468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 201 AA; 23017 MW; C3441BC5259AB3D CRC64;

Query Match 100.0%; Score 35; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 190 PPOFSY 195

RESULT 7
Q9PUJ3_CHICK PRELIMINARY; PRT; 246 AA.
AC Q9PUJ3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Protein serine/threonine kinase (Fragment).

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GN Name=AKT2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA MEDLINE=21218646; PubMed=11319165;
RA Johnson A.L., Bridgham J.T., Swenson J.A.;
RT "Activation of the Akt/protein kinase B signaling pathway is
RT associated with granuloa cell survival.";
RL Biol. Reprod. 64:1566-1574(2001).

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EMBL; AF181260; AAD54413.1; -; mRNA.
DR HSSP; P31751; IMRY.
DR SMR; Q9PUJ3; 1-228.
DR Ensembl; ENSGALG0000011620; Gallus gallus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:000468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 246 AA; 28570 MW; CCAFAA3BBEIDBED CRC64;

Query Match 100.0%; Score 35; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 235 PPOFSY 240

RESULT 8
Q9NS82_CAEEL PRELIMINARY; PRT; 256 AA.
AC Q9NS82;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 2.
DT 07-FEB-2006, entry version 30.
DE Hypothetical protein.
GN ORFNames=Y119CIA.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Briscot N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:

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CC 01670:eva-1; NbExp=1; IntAct=EBI-315836, EBI-311862;
CC 020485:466g11.1; NbExp=1; IntAct=EBI-315836, EBI-322655;
CC 022534:sei-16; NbExp=1; IntAct=EBI-315836, EBI-327662;
CC 091238:sei-4; NbExp=1; IntAct=EBI-315836, EBI-329192;
CC 019969:ima-3; NbExp=1; IntAct=EBI-315836, EBI-317340;
CC 090989:jic-1; NbExp=1; IntAct=EBI-315836, EBI-318513;
CC 045521:thr-111; NbExp=1; IntAct=EBI-315836, EBI-313336;
CC 009485:py-1; NbExp=1; IntAct=EBI-315836, EBI-315739;
CC 045784:cal-9; NbExp=1; IntAct=EBI-315836, EBI-327711;
CC 017359:vab-3; NbExp=1; IntAct=EBI-315836, EBI-319610;
CC -----
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CC -----
DR EMBL: AC006709; AAF60432.2; -; Genomic_DNA.
DR IntAct: Q9N582; -
DR Ensembl: Y119C1A.1; Caenorhabditis elegans.
DR Wormbase: WBGene0002466; Y119C1A.1.
DR WormRep: Y119C1A.1; CE34395.
DR GO: GO:0005515; F:protein binding; IPI.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR001876; ZnF_RanBP2.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
DR PROSITE: PS01358; ZF_RANBP2_1; 1.
DR PROSITE: PS50199; ZF_RANBP2_2; 1.
SQ Complete proteome; Hypothetical protein.
SQ SEQUENCE 256 AA; 28520 MM; DD279034AAAF77382 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PROFSY 6
Db 23 PROFSY 28

RESULT 9
QATBD9_TETNG PRELIMINARY; PRT; 302 AA.
ID QATBD9_TETNG
AC QATBD9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Chromosome undetermined SCAF7139, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0003798001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Necteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castelli V., Kalinka M., Vachere B.,
RA Biemond C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
RA Cnuand C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Keills M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schacher V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetradon nigriviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
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CC -----
DR EMBL: CAAB01007139; CAF89793.1; -; Genomic_DNA.
DR QATBD9; 40-235.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00106; PROTEIN_KINASE_ST; 1.
DR KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 302
FT SEQUENCE 302 AA; 34209 MM; 32D4564122D5855F CRC64;

Query Match 100.0%; Score 35; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PROFSY 6
Db 291 PROFSY 296

RESULT 10
Q8CE74_MOUSE PRELIMINARY; PRT; 353 AA.
ID Q8CE74_MOUSE
AC Q8CE74;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 10 days neonate skin cDNA, RIKEN full-length enriched library,
DE clone:4732465F20 product:chymoma viral proto-oncogene 2, full insert
DE sequence. (Fragment).
GN Name=Akt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Skin;
RX MBLINK=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard D., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Walting L.G., Adkins V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banerji M., Baxter K., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Chowdhury V., Christoffels A., Cluttenbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Haberer M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motenagu-Tobar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Tesard R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuoka S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashima T.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nishimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tasigi M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=2254663; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okaaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nikaido I., Oosato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake U.A., Bradt D., Brusic V., Chochua C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Tesard R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirokawa-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyakoshi A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Asahara M., Batalov S., Casavant T.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake U., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-699(2001).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takada Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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CC -----
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CC -----
DR EMBL: AK028671; BAC26162.1; -; mRNA.
DR HSSP: P31751; 1MRV.
DR Ensembl: ENSMUSG00000004056; Mus musculus.
DR MGI: MGI:104874; Akt2.
DR GO: GO:0030027; C:lamellipodium; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0046328; F:regulation of JNK cascade; IDA.
DR InterPro: IPR000961; Kinase_C.
DR InterPro: IPR008271; Ser_Ehr_kin_AS.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00433; Kinase_C; 1.
DR Pfam: PF00069; Kinase; 1.
DR Prodom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_X; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
KM NON_TER 1
SQ SEQUENCE 353 AA; 40766 MW; 325D23F43975FFD7 CRC64;

OY 1 FPOFSY 6
Db 342 FPOFSY 347

Query Match 100.0%; Score 35; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
ID 0519W5_CANFA PRELIMINARY; PRT; 419 AA.
AC 0519W5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protein kinase B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu P., Colitz C.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AY83721; AAW52726.1; -; mRNA.
DR SMR: 0519W5; 1-49.
DR Ensembl: ENSCARG00000005388; Canis familiaris.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001849; PH.
DR InterPro: IPR01993; PH_type.
DR InterPro: IPR000961; Kinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Kinase; 1.

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DR Pfam: PF00433; Kinase_C; 1.
DR Prodom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_X; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KM Kinase.
SQ SEQUENCE 419 AA; 48357 MW; 14CE64B62F7043C CRC64;

OY 1 FPOFSY 6
Db 408 FPOFSY 413

Query Match 100.0%; Score 35; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
ID 04SLA7_TETNG PRELIMINARY; PRT; 472 AA.
AC 04SLA7;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Chromosome 7 SCF14557, whole genome shotgun sequence.
GN ORFNames=GSTENG00016324001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dadiyva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vachere B.,
RA Blumont C., Skalli Z., Catolico L., Poulin J., De Berardinis V.,
RA Cruaud C., Duprat S., Broitier P., Courneau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt J.-N., Guigo R., Zody M.C., Westrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weisenbach J., Roest Crollius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
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CC -----

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DR EMBL; CAE01014557; CAF98575.1; -; Genomic_DNA.
 DR SMR; Q4SLA7; 1-103.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 472 AA; 54836 MW; F9448E88D55273B CRC64;

Query Match 100.0%; Score 35; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
 Db 461 PPOFSY 466

RESULT 13
 ID Q802Y3_BRARE PRELIMINARY; PRT; 478 AA.
 AC Q802Y3;
 DT 01-JUN-2003 integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003 sequence version 1.
 DT 07-FEB-2006 entry version 24.
 DE V-akt murine thymoma viral oncogene homolog 2, like.
 GN Name=akt21;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]_Nucleotide sequence.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Manuina K., Farnier A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madañ A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smillius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."/;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=whole body;
 RA Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 1 PH domain.

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DR EMBL; BC046892; AAH46892.1; -; mRNA.
 DR HSSP; P31751; IMRV.
 DR SMR; Q802Y3; 1-111.
 DR Ensembl; ENSDARG0000026797; Danio rerio.
 DR ZFIN; ZDB-GENE-040121-5; akt21.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 478 AA; 55452 MW; F7B5AB68428A7A6A CRC64;

Query Match 100.0%; Score 35; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
 Db 467 PPOFSY 472

RESULT 14
 ID AKT3_HUMAN STANDARD; PRT; 479 AA.
 AC Q9Y243; Q960V3; Q9UPP5;
 DT 01-DEC-2000 integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999 sequence version 1.
 DT 07-MAR-2006 entry version 59.
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 GN (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STR-2).
 GN Name=AKT3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND MUTAGENESIS.
 RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;

RA Brodbeck D., Cron P., Hemmings B.A.;
 RT "A human protein kinase B gamma with regulatory phosphorylation sites
 in the activation loop and in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 274:9133-9136(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=99255329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;
 RA Nakatani K., Sakae H., Thompson D.A., Weigelt R.J., Roth R.A.;
 RT "Identification of a human Akt3 (protein kinase B gamma) which
 contains the regulatory serine phosphorylation site.";
 RL Biochem. Biophys. Res. Commun. 257:906-910(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=99421751; PubMed=10491192;
 RA Masuie S., Haefliger B., Weeslink J.-J., Hoefnagel E., Mortier E.,
 Verhaesselt P., Tuytelaars A., Gordon R., Richardson A.;
 RT "Molecular cloning, expression and characterization of the human
 serine/threonine kinase Akt-3.";
 RL Eur. J. Biochem. 265:353-360(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RA Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;
 RT "Cloning of a novel human cDNA, STR-2, which encodes a rat serine-
 threonine protein kinase (STR) homolog.";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
 RC TISSUE=Testis;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wemmann S., Weill B., Wellenreuther R., Gassenhuber J., Glaesl S.,
 Ansoorge W., Boecker M., Bioecker H., Bauersachs S., Blum H.,
 Lauber J., Dueserhoef A., Beyer A., Koehner K., Strack N.,
 Mewes H.-W., Ottensmeyer F., Obermaier B., Tampe J., Heubner D.,
 Wandt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND MUTAGENESIS OF
 THR-305 AND THR-447.
 RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
 RA Brodbeck D., Hill M.M., Hemmings B.A.;
 RT "Two splice variants of PKB gamma have different regulatory capacity
 depending on the presence or absence of the regulatory phosphorylation
 site Ser-472 in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 276:29550-29558(2001).
 CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 role in regulating cell survival. Capable of phosphorylating
 several known proteins. Truncated isoform 2/PKB gamma 1 without
 the second serine phosphorylation site could still be stimulated
 but to a lesser extent.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- INTERACTION:
 CC Q16543: CDC37, NBEXP=1, Intact=EBI-296115, EBI-295634;
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 cell stimulation leading to its translocation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=PKB gamma;
 CC IsoId=O9Y243-1; Sequence=Displayed;
 CC Name=2; Synonyms=PKB gamma 1;
 CC IsoId=O9Y243-2; Sequence=VSP_004947;
 CC -1- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in
 brain, lung and kidney, but weakly in heart, testis and liver. In
 fetal tissues, it is highly expressed in heart, liver and brain
 and not at all in kidney.
 CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 kinase alpha (PI(3)K) results in its targeting to the plasma
 membrane.
 CC -1- PTM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both serines and threonines is required for
 full activity.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 subfamily.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -----
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 CC -----
 DR EMBL: AF124141; AAD29089.1; -; mRNA.
 DR EMBL: AF135794; AAL40196.1; -; mRNA.
 DR EMBL: AF085234; AAL40392.1; -; mRNA.
 DR EMBL: AJ245709; CAB53537.1; -; mRNA.
 DR EMBL: AL117525; CAB55977.1; ALT TERM; mRNA.
 DR EMBL: AY005799; AAF91073.1; -; mRNA.
 DR PIR: A59380; A59380.
 DR HSP: P31751; IGZK.
 DR SMR: Q9Y243; 1-115.
 DR IntAct: Q9Y243; -.
 DR Ensembl: ENSG00000117020; Homo sapiens.
 DR HGNC: HGNC:393; AKT3.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0004672; F:protein kinase activity; TAS.
 DR GO: GO:000468; F:protein amino acid phosphorylation; TAS.
 DR GO: GO:007165; P:signal transduction; TAS.
 DR InterPro: IPR011849; PH.
 DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Protein kinase.
 DR InterPro: IPR008271; Ser_Thr_kin_AS.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PSS0003; PH DOMAIN; 1.
 DR PROSITE: PSS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PSS0108; PROTEIN KINASE ST; 1.
 DR KMW: Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
 KM Phosphorylation; Serine/threonine-protein kinase; Transferase.
 FT CHAIN 1 479
 FT RAC-gamma serine/threonine-protein
 FT kinase
 FT /FTId=PRO_0000085611.
 FT PH.
 FT protein kinase.
 FT ATP (By similarity).
 FT Proton acceptor (By similarity).
 FT BINDING 177 177
 FT ATP (By similarity).
 FT MOD_RES 305 305
 FT Phosphothreonine (By similarity).
 FT MOD_RES 472 472
 FT Phosphoserine (By similarity).
 FT VARSPPLIC 452 479
 FT YDSDGMDMDNERPDPQPSASGRE -> CQSDCGML
 FT GNMWK (in isoform 2).
 FT /FTId=VSP_004947.
 FT T->A: No activation after pervanadate
 FT treatment.
 FT T->D: 2-fold increase of phosphorylation
 FT steady state level, no activation after
 FT pervanadate treatment.
 FT T->A: No effect.
 FT T->D: 67% decrease of activity after
 FT pervanadate treatment.
 FT S->D: 1.4-fold increase of
 FT phosphorylation steady state level, 50%
 FT decrease of activity after pervanadate
 FT treatment.
 FT SEQUENCE 479 AA; 55775 MW; F08BDBE502E78FB CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 75;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPOFSY 6
 |||||
 Db 468 PPOFSY 473

RESULT 15
 AKT3 MOUSE
 ID AKT3 MOUSE STANDARD; PRT; 479 AA.
 AC Q9WUA6;
 DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999, sequence version 1.
 DT 07-MAR-2006, entry version 50.
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 GN (Protein kinase Akt-3) (protein kinase B, gamma) (PKB gamma).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE:99194749; PubMed=10092563; DOI=10.1074/jbc.274.14.9133;
 RA Brobeck D., Cron P., Hemmings B.A.;
 RT "A human protein kinase B gamma with regulatory phosphorylation sites
 in the activation loop and in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 274:9133-9136(1999).
 CC [2]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RA PubMed=11387345; DOI=10.1074/jbc.M104633200;
 RX Brobeck D., Hill M.M., Hemmings B.A.;
 RT "Two splice variants of PKB gamma have different regulatory capacity
 depending on the presence or absence of the regulatory phosphorylation
 site Ser-472 in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 276:29550-29558(2001).
 CC -I- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 role in regulating cell survival. Capable of phosphorylating
 several known proteins. Truncated isoform 2/PKB gamma 1 without
 the second serine phosphorylation site could still be stimulated
 but to a lesser extent (By similarity).
 CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 cell stimulation leading to its translocation.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=PKB gamma;
 CC IsoId=Q9WUA6-1; Sequence=Displayed;
 CC Name=2; Synonyms=PKB gamma 1;
 CC IsoId=Q9WUA6-2; Sequence=VSP_004948;
 CC -I- TISSUE SPECIFICITY: Isoform 1 is expressed in prostate, testis,
 uterus and mammary gland and isoform 2 is expressed in prostate,
 testis and mammary gland.
 CC -I- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 kinase alpha (PI3K) results in its targeting to the plasma
 membrane.
 CC -I- PTM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both sites is required for full activity.
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 subfamily.
 CC -I- SIMILARITY: Contains 1 PH domain.
 CC -----
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 CC -----
 CC EMBL: AF124142; AAD29090.1; -; mRNA.
 CC HSSP: P31751; IGZK.
 CC SMR: Q9WUA6; 1-115.
 CC DR Ensembl: ENSMUSG0000019699; Mus musculus.
 CC MGI: MGI:1345147; Akt3.
 CC InterPro: IPR001849; PH.

DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Kinase C.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser_thr_kin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00433; Kinase C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS50003; PH DOMAIN; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
 KW Phosphorylation; Serine/threonine-protein kinase; Transferase;
 CHAIN 1 479 RAC-gamma serine/threonine-protein kinase.
 FT /FTId=PRO_0000085612.
 FT DOMAIN 5 107 PH.
 FT 148 405 Protein kinase.
 FT NP_BIND 154 162 ATP (By similarity).
 FT ACT_SITE 271 271 Proton acceptor (By similarity).
 FT BINDING 177 177 ATP (By similarity).
 FT MOD_RES 305 305 Phosphothreonine (By similarity).
 FT MOD_RES 472 472 Phosphoserine (By similarity).
 FT VARSP_LIC 452 479 YDDGMDGMDNRRRPHPPQFSYSASGR -> CQOSDCGML
 FT FT GWKKNDNRK (in isoform 2).
 FT /FTId=VSP_004948.
 SQ SEQUENCE 479 AA; 55714 MW; F08ACDF5743B8FB CRC64;

Query Match 100.0%; Score 35; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPOFSY 6
 |||||
 Db 468 PPOFSY 473

Search completed: June 14, 2006, 02:16:28
 Job time : 220 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:58 ; Search time 218 Seconds
(without alignments): 25.459 Million cell updates/sec

Title: 09937009-A
Perfect score: 36
Sequence: 1 frdfdy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	60	2	06PSW9 HUMAN
2	36	100.0	234	2	066WK2 FELIX
3	36	100.0	389	2	06CIS7 TRYICR
4	36	100.0	389	2	0580R7 TRYRYP
5	36	100.0	392	2	042262 XENLA
6	36	100.0	539	2	03GY02 NACTO
7	36	100.0	585	2	097KY8 CLOAB
8	36	100.0	786	1	TIR1 HUMAN
9	36	100.0	786	2	032MK3 HUMAN
10	36	100.0	786	2	032MK4 HUMAN
11	36	100.0	786	2	05FMG5 HUMAN
12	36	100.0	786	2	06F164 HUMAN
13	36	100.0	796	2	04LDR7 PIG
14	36	100.0	796	2	059HT9 PIG
15	36	100.0	966	2	04RZS3 TETNG
16	36	100.0	984	1	PKN2 HUMAN
17	33	91.7	114	2	05A758 CANAL
18	33	91.7	142	2	05A7D3 CANAL
19	33	91.7	168	2	094044 CANAL
20	33	91.7	210	2	025450 HELPY
21	33	91.7	235	2	092L88 HELPY
22	33	91.7	254	2	09XY00 RHYPD
23	33	91.7	261	2	07NS51 PHOLA
24	33	91.7	348	2	08MU12 PHILA
25	33	91.7	352	1	LARK DROME
26	33	91.7	434	1	KE51 YEAST
27	33	91.7	434	1	06C5T1 YEAST
28	33	91.7	437	2	02V2Y4 ANATH
29	33	91.7	437	2	06FJ22 CANGA
30	33	91.7	464	1	MOC3 ARATH
31	33	91.7	511	2	08YV02 ANASP

32	33	91.7	529	2	09FK32 ARATH	09FK32 arabidopsis
33	33	91.7	598	2	05AID5 CANAL	05AID5 candida alb
34	33	91.7	611	2	02QNT3 TORNA	02QNT3 oryza sativ
35	33	91.7	611	2	05MA08 ARATH	05MA08 arabidopsis
36	33	91.7	613	2	09LNX4 ARATH	09LNX4 arabidopsis
37	33	91.7	664	1	04F8B2 CLOPE	04F8B2 clostridium
38	33	91.7	724	2	04F8B8 PELUB	04F8B8 pelagibacte
39	33	91.7	724	2	02UNN2 ASPOR	02UNN2 aspergillus
40	33	91.7	870	2	054Q71 DICI	054Q71 dictyosteli
41	33	91.7	881	2	081L19 PLAF7	081L19 plasmodium
42	33	91.7	881	2	09BKN8 PLAF7	09BKN8 plasmodium
43	33	91.7	895	1	PL0D MIMIV	05GK3 mimivirus
44	33	91.7	993	1	NISB LACTA	P20103 lactococcus
45	33	91.7	993	2	048673 PLACT	048673 lactococcus

ALIGNMENTS

RESULT 1
ID 06PSW9 HUMAN PRELIMINARY; PRT; 60 AA.
AC 06PSW9;
DT 05-JUL-2004, integrated into UniprotKB/TREMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE PKN2 protein.
GN Name=PKN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stedlecken M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Toehiyuki S., Carninci P., Prange C.J.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BC062620; AA62620.1; -; mRNA.
CC Ensemble: ENSG0000065243; Homo sapiens.
CC GO: GO:0005524; F:ATP binding; IEA.
CC GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
CC GO: GO:000468; F:Protein amino acid phosphorylation; IEA.
CC InterPro: IPR000961; Kinase_C.
CC Pfam: PF00433; Kinase_C; 1.

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DR SMART; SM00133; S.TK.X; 1.
SQ SEQUENCE 60 AA; 7149 MW; 6CB26D2FB270F7D7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
   |||||
Db 50 FRDPDY 55

RESULT 2
O66WK2_FELCA PRELIMINARY; PRT; 234 AA.
AC O66WK2;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE Toll-like receptor 1 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15963821; DOI=10.1016/j.yetimm.2005.02.022;
RA Ignacio G., Nordone S., Howard K.E., Dean G.A.;
RT "Toll-like receptor expression in feline lymphoid tissues.";
RL Vet. Immunol. Immunopathol. 106:229-237(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Ignacio G., Dean G.A.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY00368; AAU12171.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 27070 MW; DDD466BDD601BCE CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 234;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
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Db 105 FRDPDY 110

RESULT 3
O4CT57_TRYCR PRELIMINARY; PRT; 389 AA.
AC O4CT57;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Trypophanyl-tRNA synthetase, putative (EC 6.1.1.2).
GN ORFNames=TC00.1047053510647.30;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Schizotrypanum
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;

```

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RA El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA Blandin G., Westenberg S.J., Caler E., Cerqueira G.C., Branche C.,
RA Haas B., Anupama A., Arner E., Aslund L., Atcioglu P., Bontempi E.,
RA Bringard F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA Englund P.T., Fazellina G., Feldblum T., Ferreira M., Frasch A.C.,
RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA Nelson S., Ochaya S., Osogawa K., Pal G., Parsons M., Pentony M.,
RA Petersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA Fraser C.M., Stuart K.D., Anderson B.,
RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RL Disease.";
RN Science 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Bader J.,
RA Bringard F., Cadag E., Carlson J.M., Cerqueira G.C., Greasy T.,
RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA Salzberg S.L., Shallow N., Silva J.C., Sundaram J., Westenberg S.,
RA White O., Melville S.E., Donelson J.E., Anderson B., Stuart K.D.,
RA Hall N.;
RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL Science 0:0-0(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N., Bartholomeu D., Haas B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DR EMBL; AAHK01001949; EAN83677.1; -, Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO; GO:0006436; P:tryptophan-tRNA aminoacylation; IEA.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp_tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA_tRNA_ligase_1; UNKNOWN_1.
KM Aminoacyl-tRNA synthetase, ligase.
SQ SEQUENCE 389 AA; 44316 MW; A1F94B797CC42FD8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 389;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
   |||||
Db 152 FRDPDY 157

RESULT 4
O580R7_9TRYP PRELIMINARY; PRT; 389 AA.
AC O580R7;

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DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Trypophanyl-tRNA synthetase, putative (EC 6.1.1.2).
 GN ORFNames=TB927.3.5580;
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallem J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalek H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA El-Sayed N.M., Khalek H., Adams M.D.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Haas B., Blandin G., El-Sayed N.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AC093543; AAX81067.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016874; F:Ligase activity; IEA.
 DR GO: GO:0004830; F:Trypophan-tRNA ligase activity; IEA.
 DR GO: GO:0006436; F:Trypophanyl-tRNA aminoacylation; IEA.
 DR InterPro: IPR002305; tRNA-synt_1b.
 DR InterPro: IPR001412; tRNA-synt_1b.
 DR InterPro: IPR002306; TRP-tRNA-synt_1b.
 DR Pfam: PF00579; tRNA-synt_1b; 1.
 DR PRINTS: PRO1039; TRNASYNTTRP.
 DR TIGRFAMs: TIGR00233; trps; 1.
 DR PROSITE: PS00178; AA tRNA_LIGASE_I; UNKNOWN_1.
 DR Anticodon-tRNA synthetase; ligase.
 SQ SEQUENCE 389 AA; 44246 MW; F887BP8A066CA27 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 |||||
 DB 152 FRDPDY 157

RESULT 5
 042262_XENLA PRELIMINARY; PRT; 392 AA.
 AC 042262;
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 28.
 DE Protein kinase C-related kinase 2 (Fragment).
 GN Name=PRK2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98037762; PubMed=9368003; DOI=10.1074/jbc.272.47.29449;
 RA Cryns V.L., Byun Y., Rana A., Mellor H., Lustig K.D., Ghannem L.,

RA Parker P.J., Kirschner M.W., Yuan J.;
 RT "Specific proteolysis of the kinase protein kinase C-related kinase 2
 RT by caspase-3 during apoptosis. Identification by a novel, small pool
 RT expression cloning strategy.";
 RL J. Biol. Chem. 272:29449-29453 (1997).
 CC 1 - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 DR EMBL: AF027183; AAC13357.1; -; mRNA.
 DR HSSP: P31751; IMRY.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0001066; F:nucleotide binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000961; Kinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Kinase_C; 1.
 DR Pfam: PF00433; Kinase_C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR Arp-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 392 AA; 44960 MW; 76891B23ABC3C87 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 |||||
 DB 382 FRDPDY 387

RESULT 6
 03GY02_9ACTO PRELIMINARY; PRT; 539 AA.
 AC 03GY02;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE AMP-dependent synthetase and ligase.
 GN ORFNames=NocADRAFT_1748;
 OS Nocardioides sp. JS614.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Propionibacteriaceae; Nocardioidaceae; Nocardioides.
 NCBI_TaxID=196162;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JS614;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Istrati S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Nocardioides sp.
 RT JS614.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JS614;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Nocardioides sp. JS614.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.

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CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC -----
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CC -----
DR EMBL: AA1801000046; EAO06609.1; -; Genomic_DNA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF0501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
KW ligase.
SQ SEQUENCE 539 AA; 59725 MW; B6976197A620CFB CRC64;

Query Match 100.0%; Score 36; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 131 FRDPDY 136

RESULT 7
ID Q97KY8_CLOAB PRELIMINARY; PRT; 585 AA.
AC Q97KY8;
DT 01-OCT-2001, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE ATP-dependent RNA helicase, superfamily II.
GN OrderedocNames=CAC0778;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.V., Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -----
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CC -----
DR EMBL: AE007593; AAK78754.1; -; Genomic_DNA.
DR PIR: G96995; G96995.
DR BioCyc: CAC01488; CAC0778-MONOMER; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:000166; F:nucleotide binding; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 585 AA; 68643 MW; 849DFD42485D593 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 585;

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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 54 FRDPDY 59

RESULT 8
ID TLRL_HUMAN STANDARD; PRT; 786 AA.
AC Q1539; Q15452; Q9UG90;
DT 31-JAN-2002, integrated into UniProtKB/Swiss-Prot.
DT 31-JAN-2002, sequence version 2.
DT 07-MAR-2006, entry version 57.
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like
DE protein) (TIR) (CD281 antigen).
GN Name=TLRL1; Synonyms=K1AA0012;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Erythrocytopenia;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RA "A family of human receptors structurally related to Drosophila
RT Toll.",
RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026; DOI=10.1093/dnares/1.1.27;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RL DNA Res. 1:27-35(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansorge W., Boecker M., Bloeker H., Bauesachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Oeltgenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [4]
RP PROTEIN SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RA Xu Y., Tao X., Shen B., Horng T., Medhlov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domains.";
RL Nature 408:111-115(2000).
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MYD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (by similarity).

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CC -1- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 8 LRR (leucine-rich) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
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CC -----
DR EMBL: U88540; AAC34137.1; -; mRNA.
DR EMBL: D13637; BAA02801.2; ALT_INTT; mRNA.
DR EMBL: AL050262; CAB3364.1; -; mRNA.
DR PIR: T08664; T08664.
DR PDB: 1FYV; X-ray; A=625-785.
DR Ensemble: ENSG00000174125; Homo sapiens.
DR H-invDB: HIX0004160; -.
DR HGNC: HGNC:11847; TLR1.
DR MIM: 601194; gene.
DR GO: GO:0005887; C:Integral to plasma membrane; TAS.
DR GO: GO:0045335; C:phagocytic vesicle; ISS.
DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0042487; F:transmembrane receptor activity; NAS.
DR GO: GO:0007250; F:activation of NF-kappaB-inducing kinase; ISS.
DR GO: GO:0042455; P:detection of triacylated bacterial lipoprotein; ISS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0045416; P:macrophage activation; NAS.
DR GO: GO:0042535; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR004075; IL1_rcpt_1.
DR InterPro: IPR001611; LRR_C.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_CYP.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR01537; INTRLNRI1F.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR 3D-structure: Direct protein sequencing; Glycoprotein;
KM Immune response; Inflammatory response; Innate immunity;
KM Leucine-rich repeat; Membrane; Polymorphism; Receptor; Repeat; Signal;
KM Transmembrane.
FT CHAIN 1 24
FT SIGNAL 1 786
FT TOPO_DOM 25 580
FT TRANSMEM 581 601
FT TOPO_DOM 602 786
FT REPEAT 68 91
FT REPEAT 91 113
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FT FT CONFLICT 248 248 N -> S (in Ref. 3).
FT FT CONFLICT 276 276 S -> N (in Ref. 2).
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FT FT STRAND 631 633
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FT FT HELIX 762 764
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FT FT SEQUENCE 786 AA; 90290 MW; 1406C60FB5847F58 CRC64;

Query Match 100.0%; Score 36; DB 1; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 9
O32MK3 HUMAN PRELIMINARY; PRT; 786 AA.
ID O32MK3 HUMAN
AC O32MK3
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
GN Toll-like receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC109094; AA109095.1; -; mRNA.
 CC GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 KW Receptor.
 KM SEQUENCE 786 AA; 90290 MW; 1406C60FB5847F58 CRC64;
 SQ

Query Match 100.0%; Score 36; DB 2; Length 786;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDFDY 6
 Db 289 FRDFDY 294

RESULT 10
 Q32MK4 HUMAN PRELIMINARY; PRT; 786 AA.
 ID Q32MK4;
 AC Q32MK4;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Toll-1-like receptor 1.
 GN Name=TLR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=PCR rescued clones;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC109093; AA109094.1; -; mRNA.
 CC GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 KW Receptor.
 KM SEQUENCE 786 AA; 90291 MW; 1BFCC5E42EA5242 CRC64;
 SQ

Query Match 100.0%; Score 36; DB 2; Length 786;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDFDY 6
 Db 289 FRDFDY 294

RESULT 11
 Q5FWG5 HUMAN PRELIMINARY; PRT; 786 AA.
 ID Q5FWG5;
 AC Q5FWG5;
 DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Toll-1-like receptor 1.
 GN Name=TLR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=lymph;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

GenCite version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:09:23 / Search time 24 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: 09937009-A

Perfect score: 36

Sequence: 1 frdfdy 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 80.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	585	2	G96995	ATP-dependent RNA
2	36	100.0	786	2	T08664	Toll protein-like
3	36	100.0	984	2	S67527	protein kinase (EC
4	33	91.7	168	2	T18236	protein-tyrosine-P
5	33	91.7	210	2	G64614	molybdopterin bios
6	33	91.7	235	2	D71901	hypothetical prote
7	33	91.7	434	2	S42676	KSI protein - yea
8	33	91.7	511	2	AE2078	ferriochrome-iron r
9	33	91.7	993	2	C31915	lanthiolic nisin
10	32	88.9	281	2	PC4220	protein kinase (EC
11	32	88.9	886	2	JC7083	protein kinase (EC
12	32	88.9	949	2	UC2130	protein kinase (EC
13	32	88.9	1120	2	S67208	hypothetical prote
14	32	88.9	1849	2	T00415	hypothetical prote
15	31	86.1	238	2	T24899	hypothetical prote
16	31	86.1	247	1	KYHUCM	chymase (EC 3.4.21
17	31	86.1	525	2	T13926	hypothetical prote
18	31	86.1	1428	2	T13926	probable protein P
19	30	83.3	222	2	G64363	deoxyritydylate hyd
20	30	83.3	298	2	T23435	hypothetical prote
21	30	83.3	328	2	H97089	uncharacterized AT
22	30	83.3	363	2	F69325	first mannosyl tra
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24	30	83.3	384	2	T23604	hypothetical prote
25	30	83.3	390	1	B86790	probable exonuclea
26	30	83.3	402	2	S58477	rdel protein - fis
27	30	83.3	408	2	G96500	hypothetical prote
28	30	83.3	425	2	E69551	thiamin biosynthes
29	30	83.3	446	2	A64940	pmba protein limpo

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32	30	83.3	515	2	F70128	transcription term
33	30	83.3	644	2	T10403	p74 protein - Orgy
34	30	83.3	645	1	WMNV74	p74 protein - Auto
35	30	83.3	645	2	C72867	occlusion-derived
36	30	83.3	645	2	S29849	gene p74 protein -
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38	30	83.3	681	2	E88158	protein C17G10.4c
39	30	83.3	708	2	T34098	hypothetical prote
40	30	83.3	715	2	B83222	regulatory protein
41	30	83.3	775	2	T45238	probable transfera
42	30	83.3	789	2	A70868	probable p18B2 - M
43	30	83.3	1042	1	GBRCE	beta-galactosidase
44	30	83.3	1042	2	E85968	evolved beta-D-gal
45	30	83.3	1042	2	F91123	evolved beta-D-gal

ALIGNMENTS

RESULT 1

G96995

ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: G96995

R:Noiling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: G96995

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-585 <KUR>

A:Cross-references: UNIPROT:Q97KY8; UNIPARC:UPI00000C9F97; GB:AE001437; PIDN:AAK78754.1;

A:Experimental source: Clostridium acetobutylicum ATCC6824

C:Genetics:

A:Gene: CAC0778

Query Match

Best Local Similarity 100.0%; Score 36; DB 2; Length 585;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 FRDFDY 59

RESULT 2

T08664

Toll protein-like receptor DKFZp547I0610.1 - human

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T08664

R:Postek, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16466

A:Accession: T08664

A:Molecule type: mRNA

A:Residues: 1-786 <POU>

A:Cross-references: UNIPROT:Q15399; UNIPARC:UPI000016AC46; EMBL:AL050262

A:Experimental source: fetal brain; clone DKFZp547I0610

C:Genetics:

A:Note: DKFZp547I0610.1

Query Match

Best Local Similarity 100.0%; Score 36; DB 2; Length 786;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 FRDFDY 6

|||||

Db 289 FRDPDY 294

RESULT 3

567527

protein kinase (EC 2.7.1.-) PKR2 - human

C/Species: Homo sapiens (man)

C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Oct-2004

C/Accession: S67527; I67464

R/Palmer, R.H.; Ridden, J.; Parker, P.J.

Eur. J. Biochem. 227, 344-351, 1995

A/Title: Cloning and expression patterns of two members of a novel protein-kinase-C-related

A/Reference number: I53527; MUID:95154310; PMID:7851406

A/Accession: S67527

A/Molecule type: mRNA

A/Residues: 1-984 <PRL>

A/Cross-references: UNIPROT:Q16513; UNIPARC:UPI0000040291; EMBL:S75548; NID:g914099; PII

A/Experimental source: fetal brain

A/Accession: I67464

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-984 <RES>

A/Cross-references: UNIPARC:UPI0000040291; GB:S75548; NID:g914099; PIDN:AMB33346.1; PID

C/Keywords: ATP; phosphotransferase

F/555-916/Domain: protein kinase homology <KIN>

F/663-671/Region: protein kinase ATP-binding motif

F/686/Active site: Lys #status predicted

Query Match 100.0%; Score 36; DB 2; Length 984;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6

Db 974 FRDPDY 979

RESULT 4

T18236 protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - yeast (Candida albicans)

C/Species: Candida albicans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18236

R/Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL data library, November 1998

A/Reference number: Z18831

A/Accession: T18236

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-168 <BAR>

A/Cross-references: UNIPROT:O94044; UNIPARC:UPI000006A0FC; EMBL:AL033501; PIDN:CAA2:994

C/Genetics:

A/Gene: 1PDI

A/Intons: 22/2

C/Superfamily: protein-tyrosine-phosphatase, low molecular weight

C/Keywords: phosphoric monoester hydrolase

Query Match 91.7%; Score 33; DB 2; Length 168;

Best Local Similarity 83.3%; Pred. No. 15;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6

Db 89 FRDPDY 94

RESULT 5

U64513

molybdopterin biosynthesis protein - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Aug-2004

C/Accession: C64614

R/Tomb, J.F.; White, O.; Kerlavape, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalek, H.G.; Glodek, A.; McKenney

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hays, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: C64614

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-210 <TCM>

A/Cross-references: UNIPROT:O25450; UNIPARC:UPI00000313A; GB:AE000588; GB:AE000511; NID

C/Genetics:

A/Start codon: TTG

C/Superfamily: Molybdopterin biosynthesis protein moeb

Query Match 91.7%; Score 33; DB 2; Length 210;

Best Local Similarity 83.3%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6

Db 92 FRDPDY 97

RESULT 6

D71901

hypothetical protein jhp0692 - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori

A/Variety: strain J99

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2004

C/Accession: D71901

R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A/Reference number: A71800; MUID:99120557; PMID:9923682

A/Accession: D71901

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-235 <ARN>

A/Cross-references: UNIPROT:Q9ZL88; UNIPARC:UPI00000D722E; GB:AE001500; GB:AE001439; NID

A/Experimental source: strain J99

C/Genetics:

A/Gene: jhp0692

C/Superfamily: Molybdopterin biosynthesis protein moeb

Query Match 91.7%; Score 33; DB 2; Length 235;

Best Local Similarity 83.3%; Pred. No. 21;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6

Db 105 FRDPDY 110

RESULT 7

S42676

KESI protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein P2614; protein YPL145C

C/Species: Saccharomyces cerevisiae

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S42676; S65156; S69042; S69454

R/Jiang, B.; Brown, J.L.; Sheraton, J.; Fortin, N.; Bussey, H.

Yeast 10, 341-351, 1994

A/Title: A new family of yeast genes implicated in ergosterol synthesis is related to the

A/Reference number: S42676; MUID:94287711; PMID:8017104

A/Accession: S42676

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-434 <CIA>

A/Cross-references: UNIPROT:P35844; UNIPARC:UPI000012DD9B; GB:U03913; NID:9433362; PIDN:

R/Punelle, B.; Cosser, F.; Goffeau, A.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65154
A:Accession: S65156
A:Molecule type: DNA
A:Residues: 1-434 <PWR>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:Z73501; NID:G1370309; PID:G247042; PID:G
A:Experimental source: strain S288C (AB972)
R:Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm.
A:Reference number: S69040
A:Accession: S69042
A:Molecule type: DNA
A:Residues: 1-434 <HBL>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:U43703; NID:G1244769; PID:G1244772; MIPS
R:Purnelle, B.; Combiez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
ogues to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
A:Reference number: S69428
A:Accession: S69454
A:Molecule type: DNA
A:Residues: 1-434 <PPW>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:X96770; NID:G1403537; PID:G239051; PID:G
C:Genetics:
A:Gene: KES1
A:Cross-references: SGD:S0006066; MIPS:YPL145C
A:Map position: 16L

Query Match 91.7%; Score 33; DB 2; Length 434;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
|:|||||
Db 362 FKDPDY 367

RESULT 8
AE2078
Ferriochrome-iron receptor [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
A:Accession: AE2078
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasa moto, S.; Watanabe, A.; Iiguchi,
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <KUR>
A:Cross-references: UNIPROT:Q8YV02; UNIPARC:UPI00000CE34D; GB:BA000019; PIDN:BAW73878.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: atx2179

Query Match 91.7%; Score 33; DB 2; Length 511;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
|:|||||
Db 304 FRDPDY 309

RESULT 9
C31915
lanthibiotic nisin biosynthesis protein nisB - *Lactococcus lactis*
N:Alternate names: probable membrane-associated protein A
C:Species: *Lactococcus lactis*
C:Date: 21-May-1990 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: S36735; C31915; C48951; C45821; B43743; S36985
R:Kuipers, O.P.; Beertthuyzen, M.M.; Sijzen, R.J.; de Vos, W.M.
Eur. J. Biochem. 216, 281-291, 1999
A:Title: Characterization of the nisin gene cluster nisABRCPA of *Lactococcus lactis*. Re
A:Reference number: S36734; MUID:93373937; PMID:7689965
A:Accession: S36735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-634, 'T', 636-993 <KUI>
A:Cross-references: UNIPROT:P20103; UNIPARC:UPI000017AC47; GB:L16226; NID:G400365
R:Buchanan, G.W.; Banerjee, S.; Hansen, J.N.
J. Biol. Chem. 263, 16260-16266, 1988
A:Title: Structure, expression, and evolution of a gene encoding the precursor of nisin,
A:Reference number: A92679; MUID:89034093; PMID:3141403
A:Accession: C31915
A:Molecule type: DNA
A:Residues: 1-63 <BUC>
A:Cross-references: UNIPARC:UPI0000170131; GB:J04057; NID:G153816; PIDN:AAA88607.1; PID:
R:Engelke, G.; Gutowski-BECKEL, Z.; Hammelmann, M.; Entian, K.D.
Appl. Environ. Microbiol. 58, 3730-3743, 1992
A:Title: Biosynthesis of the lantibiotic nisin: genomic organization and membrane locali
A:Reference number: A48951; MUID:93128945; PMID:1482192
A:Accession: C48951
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'C', 20-655, 'K', 657-894, 'T', 896-993 <ENG>
A:Cross-references: UNIPARC:UPI00001301CE; GB:X68307; GB:S52234; NID:G44040; PIDN:CAA483
A:Experimental source: strain 6F3
A:Note: sequence extracted from NCBI backbone (NCBI:122292, NCBI:122296)
R: Dodd, H.M.; Horn, N.; Gasson, M.J.
J. Gen. Microbiol. 136, 555-566, 1990
A:Title: Analysis of the genetic determinant for production of the peptide antibiotic ni
A:Reference number: A45821; MUID:90362041; PMID:2118169
A:Accession: C45821
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <DOD>
A:Cross-references: UNIPARC:UPI000017AC48; GB:M79445
R:Steen, M.T.; Chung, Y.D.; Hansen, J.N.
Appl. Environ. Microbiol. 57, 1181-1188, 1991
A:Title: Characterization of the nisin gene as part of a polycistronic operon in the chr
A:Reference number: A43743; MUID:91282469; PMID:1905517
A:Accession: B43743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840, 'VPLKLFQICLH' <STB>
A:Cross-references: UNIPARC:UPI000016F8B1; EMBL:M65089; NID:G149447; PIDN:AAV73039.1; PI
A:Note: the authors translated the codon AGC for residue 635 as Thr
C:Genetics:
A:Gene: nisB
C:Keywords: antibiotic biosynthesis; transmembrane protein
F:838-851/Domain: transmembrane #status predicted <TMM>

Query Match 91.7%; Score 33; DB 2; Length 993;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
|:|||||
Db 595 YRDPDY 600

RESULT 10
PC4220
protein kinase (EC 2.7.1.37) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Oct-2004
A:Accession: PC4220
R:Batschke, B.; Sundelin, J.
Biochem. Biophys. Res. Commun. 227, 70-76, 1996
A:Title: The mouse genes for the EPI prostanoicd receptor and the PKN protein kinase over
A:Reference number: PC4220; MUID:97011095; PMID:8858105
A:Accession: PC4220

A:Molecule type: DNA
 A:Residues: 1-281 <BAT>
 A:Cross-references: UNIPARC:UPI000017A421; GB:Y07611
 C:Comment: This protein mediates GTPase Rho dependent intracellular signalling.
 C:Genetics:

A:Gene: pgn
 A:introns: 59/2; 80/2; 106/1; 153/3; 189/3; 216/3
 C:Keywords: phosphotransferase
 F:1-213/Domain: protein kinase homology (fragment) <KIN>

Query Match 88.9%; Score 32; DB 2; Length 281;
 Best Local Similarity 83.3%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 271 FRDFDF 276

RESULT 11

JC7083
 protein kinase (EC 2.7.1.37) N beta - human

C:Species: Homo sapiens (man)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
 C/Accession: JC7083

R:Oishi, K.; Mukai, H.; Shibata, H.; Takahashi, M.; Ona, Y.

Biochem. Biophys. Res. Commun. 261, 808-814, 1999

A:Title: Identification and characterization of PKA beta, a novel isoform of protein kin

A:Reference number: JC7083; PMID:99373159; PMID:10441506

A:Accession: JC7083

A:Molecule type: mRNA

A:Residues: 1-889 <OIS>

A:Cross-references: UNIPROT:Q9UM03; UNIPARC:UPI000017A456; DDBJ:AB019692

C:Keywords: ATP; leucine zipper; phosphotransferase; protein kinase

F:557-818/Domain: protein kinase homology <KIN>

F:565-573/Region: protein kinase ATP-binding motif

F:588/Active site: Lys #status predicted

Query Match 88.9%; Score 32; DB 2; Length 889;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 676 FRDFDF 881

RESULT 12

JC2130
 protein kinase (EC 2.7.1.37) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004

C/Accession: JC2130

R:Mukai, H.; Ono, Y.

Biochem. Biophys. Res. Commun. 199, 897-904, 1994

A:Title: A novel protein kinase with leucine zipper-like sequences: Its catalytic domain

A:Reference number: JC2129; PMID:94183274; PMID:8135837

A:Accession: JC2130

A:Molecule type: mRNA

A:Residues: 1-946 <MUK>

A:Cross-references: UNIPROT:Q8V1J2; UNIPARC:UPI000017A3DF

C:Keywords: ATP; leucine zipper; phosphotransferase

F:39-66/Region: basic

F:70-290/Region: leucine zipper motif

F:517-878/Domain: protein kinase homology <KIN>

F:525-633/Region: protein kinase ATP-binding motif

F:548/Active site: Lys #status predicted

Query Match 88.9%; Score 32; DB 2; Length 946;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 676 FRDFDF 881

RESULT 13

S67208
 hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein O5648

C:Species: Saccharomyces cerevisiae

C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004

C/Accession: S67208

R:Chaplin, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobiasch, E.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67194

A:Accession: S67208

A:Molecule type: DNA

A:Residues: 1-1120 <CZI>

A:Cross-references: UNIPROT:Q08773; UNIPARC:UPI0000052F03; EMBL:Z75212; NID:G1420670; PII

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:ISW2; MIPS:YOR304w

A:Cross-references: SGD:S0005831

A:Map position: 15R

C:Superfamily: Chromatin remodelling complex ATPase chain ISWI; bromodomain homology

Query Match 88.9%; Score 32; DB 2; Length 1120;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 528 FRDFEX 533

RESULT 14

T00415
 hypothetical protein H_248015.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: T00415

R:Pillon, B.; Nhan, M.; Hawkins, J.; Beck, C.

submitted to the EMBL Data Library, September 1998

A:Description: The sequence of Homo sapiens PAC clone 248015.

A:Reference number: Z14148

A:Accession: T00415

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1849 <FUL>

A:Cross-references: UNIPROT:O14572; UNIPARC:UPI0000073A97; EMBL:AC002483; NID:G3598729; I

C:Genetics:

A:Map position: 13q12-q13

A>Note: H_248015.1

Query Match 88.9%; Score 32; DB 2; Length 1849;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 1835 FRDFDF 1840

RESULT 15

T24899
 hypothetical protein T13H5.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T24899

R:Lightning, J.

submitted to the EMBL Data Library, October 1995

A:Reference number: Z19950

A:Accession: T24899

A>Status: preliminary; translated from GB/EMBL/DDBJ

Query Match 88.9%; Score 32; DB 2; Length 1849;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
 Db 1835 FRDFDF 1840

A:Molecule type: DNA
A:Residues: 1238 <RTL>
A:Cross-references: UNIPROT:Q22470; UNIPARC:UPI00000748F0; EMBL:Z66524; PIDN:CAA91421.1
A:Experimental source: clone T13H5
C:Genetics:
A:Gene: CESP:T13H5.5
A:Map position: 2
C:introns: 33/3; 65/1; 84/3; 111/3
C:superfamily: Caenorhabditis elegans hypothetical protein T13H5.5

Query Match 86.1%; Score 31; DB 2; Length 238;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
||:||||
Db 174 FRNFDY 179

Search completed: June 14, 2006, 02:17:19
Job time : 27 secs

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CC -----
DR EMBL: BC089403; AAH89403.1; -; mRNA.
DR SMR: Q5FWG5; 625-785.
DR Ensemble1: ENSG00000174125; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR004075; IL1_Tcpl_1.
DR InterPro: IPR03016; Lipoyl_BS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_Cyp.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRCT; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 786 AA; 90267 MW; 6B9B673FE47BF3A CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 12
O6F164_HUMAN PRELIMINARY; PRT; 786 AA.
AC O6F164;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE TLR1 protein.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CR333562; CAG38593.1; -; mRNA.
DR SMR: Q6F164; 625-785.
DR Ensemble1: ENSG00000174125; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR004075; IL1_Tcpl_1.
DR InterPro: IPR03016; Lipoyl_BS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_Cyp.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRCT; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 786 AA; 90267 MW; 396C3D69B99442C4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 293 FRDPDY 298

RESULT 14
O59H19_PIG

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DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
DR PROSITE: PS50104; TIR; 1.
SQ SEQUENCE 786 AA; 90163 MW; DB6B54E6840092B4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 13
Q4LDR7_PIG PRELIMINARY; PRT; 796 AA.
AC Q4LDR7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
GN Name=TLR1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Shinkai H., Muneta Y., Suzuki K., Eguchi-Ogawa T., Awata T.,
RA Denishi H.;
RT "Complete nucleotide sequence in the porcine genomic region containing
RT Toll-like receptors 1, 6, and 10 genes and their expression
RT analysis."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: AB219564; BA06146.1; -; mRNA.
DR SMR: Q4LDR7; 629-789.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro: IPR004075; IL1_Tcpl_1.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_Cyp.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 796 AA; 90967 MW; 396C3D69B99442C4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 796;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 293 FRDPDY 298

RESULT 14
O59H19_PIG

```

```

ID  Q59H19.PIG PRELIMINARY; PRT; 796 AA.
AC  Q59H19;
DT  26-APR-2005, integrated into UniProtKB/TrEMBL.
DT  26-APR-2005, sequence version 1.
DE  07-FEB-2006, entry version 5.
GN  Toll-1-like receptor 1.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC  Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Shinkai H., Uenishi H.;
RT  "Coding sequence of porcine TLR1.";
RL  Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RA  Shinkai H., Uenishi H.;
RT  "Nucleotide sequence of porcine genomic region containing TLR1, TLR6
RT  and TLR10.";
RL  Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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-----
DR  EMBL; AB208695; BAD91798.1; -; Genomic DNA.
DR  EMBL; AB210286; BAD93714.1; -; Genomic DNA.
DR  SMR; Q59H19; 629-789.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR  InterPro; IPR004075; IL1_rcpt_1.
DR  InterPro; IPR001611; LRR.
DR  InterPro; IPR000483; LRR_C.
DR  InterPro; IPR003591; LRR_Typ.
DR  InterPro; IPR000157; TIR.
DR  Pfam; PF00560; LRR_1; 7.
DR  Pfam; PF01463; LRRCT; 1.
DR  Pfam; PF01582; TIR; 1.
DR  PRINTS; PR01537; INTRILINR1F.
DR  PRINTS; PR00019; LEURICHRPT.
DR  SMART; SM00082; LRRCT; 1.
DR  SMART; SM00255; TIR; 1.
DR  PROSITE; PS50104; TIR; 1.
DR  Receptor.
SQ  SEQUENCE 796 AA; 90948 MW; 396C38C261A642C4 CRC64;
Query Match 100.0%; Score 36; DB 2; Length 796;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 293 FRDPDY 298

```

```

RP  NUCLEOTIDE SEQUENCE.
RX  PubMed-15496914; DOI=10.1038/nature03025;
RA  Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA  Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA  Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segutens B.,
RA  Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA  Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA  Biemont C., Skali Z., Catolico L., Poulain J., De Berardinis V.,
RA  Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
RA  Parra G., Vardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA  Kellis M., Volf J.-N., Guigo R., Zody M.C., Mesirov J.,
RA  Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA  Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA  Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT  "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT  the early vertebrate proto-karyotype.";
RL  Nature 431:946-957(2004).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RG  Genoscope; Whitehead Institute Centre for Genome Research;
RL  Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
CC  -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC  cycle. It is required in higher cells for entry into S-phase and
CC  mitosis. Component of the kinase complex that phosphorylates the
CC  repetitive C-terminus of RNA polymerase II. Catalytic component of
CC  MPF (By similarity).
CC  -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC  mature oocytes (By similarity).
-----
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CC  Distributed under the Creative Commons Attribution-NonDerivs license
-----
DR  EMBL; CAE01014786; CAG06109.1; -; Genomic DNA.
DR  SMR; Q4RZS3; 119-184.
DR  GO; GO:0005622; C:intracellular; IEA.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0000166; F:nucleotide binding; IEA.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR  GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR  GO; GO:0007165; P:signal transduction; IEA.
DR  InterPro; IPR000961; Kinase C.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR000861; REM_Typ_rho_bd.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF02185; HR1; 3.
DR  Pfam; PF00069; Kinase C; 1.
DR  Pfam; PF00433; Kinase C; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00742; Hr1; 3.
DR  SMART; SM00133; S_TK_X; 1.
DR  SMART; SM00220; S_TKC; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW  ATP-binding; kinase; Nucleotide-binding;
KW  Serine/threonine-protein kinase; Transferase.
FT  NON_TER 1
FT  NON_TER 966
SQ  SEQUENCE 966 AA; 109614 MW; F74D1C73A072A4FC CRC64;
Query Match 100.0%; Score 36; DB 2; Length 966;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 956 FRDPDY 961

```

Search completed: June 14, 2006, 02:16:26

Job time : 223 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:38 ; Search time 154.5 Seconds
(without alignments)
17.756 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fptfsy 6

SEA ID No: 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	6	ABR57446 PKB activ
2	35	100.0	6	6	ABU64720 Mol1f-9pe
3	35	100.0	6	8	ADJ38822 PKB-gamma
4	35	100.0	6	8	ADJ38820 PKB-alpha
5	35	100.0	6	8	ADJ38821 PKB-beta
6	35	100.0	7	8	ADS91353 Protein k
7	35	100.0	9	3	AAV93661 PKB-alpha
8	35	100.0	10	2	AAW51736 Protein k
9	35	100.0	10	2	AAW51737 Protein k
10	35	100.0	10	8	ADQ74882 Protein k
11	35	100.0	11	3	AAV94724 Antigenic
12	35	100.0	11	4	AAW59662 Phosphory
13	35	100.0	11	8	ADR06310 Protein k
14	35	100.0	12	2	AAW34387 PKB C-ter
15	35	100.0	12	6	ABO19480 C-terminu
16	35	100.0	13	2	AAW34391 PKB resid
17	35	100.0	13	9	AED01157 DNA-prote
18	35	100.0	13	9	AED01155 DNA-prote
19	35	100.0	13	9	AED01156 DNA-prote
20	35	100.0	14	9	AED01159 PKBbeta p
21	35	100.0	14	9	AED01175 PKBalpha
22	35	100.0	14	9	AED01160 PKBbeta-M
23	35	100.0	14	9	AED01174 PKBalpha

24	35	100.0	14	9	AED01166 PKBalpha
25	35	100.0	14	9	AED01161 PKBgamma
26	35	100.0	14	9	AED01158 PKBalpha
27	35	100.0	15	2	AAW34389 Rodent PK
28	35	100.0	15	8	ADT92476 Anti-phos
29	35	100.0	16	8	ADT03822 Protein k
30	35	100.0	16	8	ADT03822 C-terminu
31	35	100.0	20	7	ADD12327 PDZ ligas
32	35	100.0	22	6	ABR57449 PKB activ
33	35	100.0	22	7	ADR92662 Peptide P
34	35	100.0	28	3	AAW13392 Human Akt
35	35	100.0	317	4	AAW99832 AGC prote
36	35	100.0	317	8	ADJ38880 PKBbeta a
37	35	100.0	318	4	AAW99831 AGC prote
38	35	100.0	318	8	ADJ38879 PKBalpha
39	35	100.0	319	4	AAW99833 AGC prote
40	35	100.0	319	8	ADJ38881 PKBgamma
41	35	100.0	335	8	ADR06326 Protein k
42	35	100.0	335	8	ADR06339 Akt1 prot
43	35	100.0	336	6	ABR57469 AGC fam11
44	35	100.0	337	10	AED32591 Human Akt
45	35	100.0	366	9	AED54161 Human ser

ALIGNMENTS

RESULT 1	ABR57446	standard; peptide; 6 AA.
ID	ABR57446	
XX	ABR57446	
AC	ABR57446	
XX	15-SEP-2003	(first entry)
DT	15-SEP-2003	
XX	PKB	activity modulating peptide #10.
DE	PKB	activity modulating peptide #10.
XX	Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;	
KW	protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;	
KW	nootropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;	
KW	structural analysis; cancer; diabetes; erectile dysfunction;	
KW	neurodegeneration.	
XX	Synthetic.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Modified-site	5 /note= "phosphoserine"
FT	Modified-site	5 /note= "phosphoserine"
XX	MO2003016516-A2.	
XX	27-FEB-2003.	
PD	27-FEB-2003.	
XX	14-AUG-2002; 2002WO-GB003735.	
PF	14-AUG-2002; 2002WO-GB003735.	
XX	14-AUG-2001; 2001GB-00019660.	
PR	01-MAY-2002; 2002GB-00009985.	
XX	(NOVS) NOVARTIS FORSCHUNGSSITFTUNG ZWEIGNIEDERL.	
PA	(CANNC-) CANCER RES INST.	
XX	Barford D, Yang J, Hemmings BA, Cron PD;	
PI	Barford D, Yang J, Hemmings BA, Cron PD;	
XX	WPI; 2003-268328/26.	
DR	WPI; 2003-268328/26.	
XX	New crystal of protein kinase B beta, useful for activating protein	
PT	kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates	
PT	or a tetragonal space group.	
XX	Claim 32; Page 265; 284pp; English.	
PS	The present invention describes a crystal of protein kinase B beta	
CC	(PKBbeta) comprising (i), where (i) comprises: (a) a tetragonal space	

CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cytosstatic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PxBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which can be used in a method from the present invention to
CC modulate PKB activity

CC
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 1 FPOFSY 6

RESULT 2
ABU64720
ID ABU64720 standard; peptide; 6 AA.
XX
AC ABU64720;
XX
DT 13-MAY-2003 (first entry)
XX
DE Motif-specific and context-independent antibody peptide antigen #143.
XX
XX Motif-specific antibody;
KM context-independent antibody. enzyme substrate identification;
KM modification state detection; enzyme inhibition; enzyme activation;
KM protein level profile; post-translation modification; phosphothreonine;
KM phosphoserine; phosphotyrosine; acetyl-lysine; nitrotyrosine;
KM kinase consensus substrate motif; protein binding motif.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002168684-A1.
XX
PD 14-NOV-2002.
XX
PF 13-NOV-2001; 2001US-00014485.
XX
PR 04-SEP-1998; 98US-00148712.
PR 24-MAR-2000; 2000US-00535364.
XX
PA (COMB/) COMB M J.
PA (TANY/) TAN Y.
PA (ZHAN/) ZHANG H.
XX
PI Comb MJ, Tan Y, Zhang H;
XX
DR WPI; 2003-298726/29.
XX
PT Producing motif-specific, context-independent antibody recognizing motif-
PT containing proteins, using a degenerate peptide library having target
PT motifs with invariant amino acids flanked by degenerate amino acids, as
PT antigens.
XX
PS Example 14; Fig 27; 86pp; English.

XX
XX The invention describes a method of producing a motif-specific, context-
CC independent antibody (1) that recognises several peptides or proteins
CC within the genome that contain motifs. The method is useful for: (1)
CC identifying an unknown substrate of an enzyme, which involves generating
CC at least one (1) which recognizes a motif common to several substrate of
CC the enzyme with a genome; (2) detecting the modification state of a
CC target substrate that contains a motif common to several substrates of an
CC enzyme within a genome; (3) screening a drug for the inhibition or
CC activation of enzyme activity on at least one substrate that contains a
CC motif common to several substrates of the enzyme within a genome; (4)
CC identifying an enzyme which modifies a known substrate that contains a
CC motif common to several substrates of the enzyme within a genome; (5)
CC profiling protein levels or post-translation modifications in a cell or
CC tissue on a genome wide scale; (6) profiling drug-induced changes in
CC protein levels or post-translation modifications in a cell or tissue on a
CC genome wide scale. The motif is selected from single phosphothreonine, a
CC single phosphoserine, a single phosphotyrosine, a single acetyl-lysine,
CC and a single nitrotyrosine, and comprises all or part of kinase consensus
CC substrate motif or a protein binding motif. This is the amino acid
CC sequence of a peptide used in the creation of a motif-specific, context-
CC independent antibody

XX
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 1 FPOFSY 6

RESULT 3
ADJ38822
ID ADJ38822 standard; peptide; 6 AA.
XX
AC ADJ38822;
XX
DT 06-MAY-2004 (first entry)
XX
DE PKB-gamma AGC hydrophobic motif peptide.
XX
XX
KM phosphoinositide dependent protein kinase 1; PKR1; molecular modelling;
KM protein kinase; catalytic domain; enzyme; hydrophobic pocket;
KM insulin signalling pathway; signalling; crystalline form;
KM protein co-ordinate data; three-dimensional structure; antifungal;
KM antidiabetic; cardiant; cytosstatic; cerebroprotective; vasotropic;
KM anorectic; protein kinase modulator; cancer; diabetes; obesity;
KM apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
KM neural injury.
XX
OS Synthetic.
XX
PN WO2003104481-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-GB002509.
XX
PR 08-JUN-2002; 2002GB-00013186.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Alessi D, Biondi R, Komander D, Van AD;
XX
DR WPI; 2004-062373/06.
XX
PT Selecting/designing compound for modulating activity of phosphoinositide
PT dependent protein kinase 1 by using molecular modelling to select/design
PT compound predicted to interact with protein kinase catalytic domain.
XX

PS Disclosure; Page 16; 383pp; English.

XX CC The present invention describes a method (M1) for selecting or designing
 CC a compound for modulating the activity of phosphoinositide dependent
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to
 CC select or design a compound that is predicted to interact with the
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is
 CC predicted to interact with the protein kinase catalytic domain. Also
 CC described: (1) selecting or designing (M2) a compound for modulating the
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 CC kinase having a hydrophobic pocket in the position equivalent to the
 CC hydrophobic pocket of human PDK1 that is defined by residues including
 CC Lys115, Ile118, Val119, Val124, Val127 and/or Leu155 of full-length human
 CC PDK1 and further having a phosphate binding pocket in the position
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
 CC (M3) the activation state of a structure for a protein kinase; (3) a
 CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1;
 CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a
 CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
 CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of
 CC a medicament for the treatment of a patient in need of modulation of
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 CC p70 S6 kinase, for example insulin signalling pathway and/or
 CC PKB1/PDK2/SGK/PRK/p70 S6 kinase/PRK2/PRK signalling; and (11) a
 CC crystalline form (VI) of polypeptide as defined in (M1). (I) has
 CC antifungal, antidiabetic, cardiant, cyostatic, cerebroprotective,
 CC vasotropic and anorectic activities, and can be used as a modulator of
 CC protein kinase. (V) is useful for modulating the ability of protein
 CC kinase to phosphorylate different substrates, e.g., different naturally
 CC occurring polypeptides, to different extents. (V) inhibits or increases
 CC the activity of protein kinase. The protein structures e.g., the co-
 CC ordinates as provided in the specification are useful for designing
 CC reagent useful in drug designing assays or characterisation of protein
 CC kinase activity or regulation. (V) capable of producing the activity of
 CC PKC, e.g., PKC beta, PKA or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 6 AA:

XX Query Match 100.0%; Score 35; DB 8; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
 QY 1 FPOFSY 6

Db 1 FPOFSY 6

RESULT 4
 ADJ38820
 ID ADJ38820 standard; peptide; 6 AA.
 XX AC ADJ38820;
 XX DT 06-MAY-2004 (first entry)
 XX DE PKA-alpha AGC hydrophobic motif peptide.
 XX KW phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;
 KW protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 KW insulin signalling pathway; signalling; crystalline form;
 KW protein co-ordinate data; three-dimensional structure; antifungal;

KW antidiabetic; cardiant; cyostatic; cerebroprotective; vasotropic;
 KW anorectic; protein kinase modulator; cancer; diabetes; obesity;
 KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 KW neural injury.

OS Synthetic.
 XX WO2003104481-A2.
 XX 18-DEC-2003.
 XX 09-JUN-2003; 2003WO-GB002509.
 XX 08-JUN-2002; 2002GB-00013186.
 XX (UYDU-) UNIV DUNDEE.
 XX Alessi D, Biondi R, Komander D, Van AD;
 XX WPI: 2004-062373/06.

DR Selecting/designing compound for modulating activity of phosphoinositide
 XX dependent protein kinase 1 by using molecular modelling to select/design
 XX compound predicted to interact with protein kinase catalytic domain.

PS Disclosure; Page 16; 383pp; English.

XX CC The present invention describes a method (M1) for selecting or designing
 CC a compound for modulating the activity of phosphoinositide dependent
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to
 CC select or design a compound that is predicted to interact with the
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is
 CC predicted to interact with the protein kinase catalytic domain. Also
 CC described: (1) selecting or designing (M2) a compound for modulating the
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 CC kinase having a hydrophobic pocket in the position equivalent to the
 CC hydrophobic pocket of human PDK1 that is defined by residues including
 CC Lys115, Ile118, Val119, Val124, Val127 and/or Leu155 of full-length human
 CC PDK1 and further having a phosphate binding pocket in the position
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
 CC (M3) the activation state of a structure for a protein kinase; (3) a
 CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
 CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a
 CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
 CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of
 CC a medicament for the treatment of a patient in need of modulation of
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 CC p70 S6 kinase, for example insulin signalling pathway and/or
 CC PDK1/PDK2/SGK/PRK/p70 S6 kinase/PRK2/PRK signalling; and (11) a
 CC crystalline form (VI) of polypeptide as defined in (M1). (I) has
 CC antifungal, antidiabetic, cardiant, cyostatic, cerebroprotective,
 CC vasotropic and anorectic activities, and can be used as a modulator of
 CC protein kinase. (V) is useful for modulating the ability of protein
 CC kinase to phosphorylate different substrates, e.g., different naturally
 CC occurring polypeptides, to different extents. (V) inhibits or increases
 CC the activity of protein kinase. The protein structures e.g., the co-
 CC ordinates as provided in the specification are useful for designing
 CC reagent useful in drug designing assays or characterisation of protein
 CC kinase activity or regulation. (V) capable of producing the activity of
 CC PKC, e.g., PKC beta, PKA or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.

SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPGFSY 6
 |||||
 1 PPGFSY 6

Db 1 PPGFSY 6

RESULT 5
 ADJ38821
 ID ADJ38821 standard; peptide; 6 AA.
 XX
 AC ADJ38821;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE PKB-beta AGC hydrophobic motif peptide.
 XX
 KM phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;
 KM protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 KM insulin signalling pathway; signalling; crystalline form;
 KM protein co-ordinate data; three-dimensional structure; antifungal;
 KM antidiabetic; cardiant; cytosolic; cerebroprotective; vasotropic;
 KM anorectic; protein kinase modulator; cancer; diabetes; obesity;
 KM apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 KM neural injury.
 KM
 XX
 OS Synthetic.
 XX
 PN W02003104481-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 09-JUN-2003; 2003WO-GB002509.
 XX
 PR 08-JUN-2002; 2002GB-00013186.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Alessi D, Biondi R, Komander D, Van AD;
 XX
 DR WPI; 2004-062373/06.
 XX
 PT Selecting/designing compound for modulating activity of phosphoinositide
 PT dependent protein kinase 1 by using molecular modelling to select/design
 PT compound predicted to interact with protein kinase catalytic domain.
 XX
 PS Disclosure; Page 16; 383pp; English.
 XX
 CC The present invention describes a method (M1) for selecting or designing
 CC a compound for modulating the activity of phosphoinositide dependent
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to
 CC select or design a compound that is predicted to interact with the
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is
 CC predicted to interact with the protein kinase catalytic domain. Also
 CC described: (1) selecting or designing (M2) a compound for modulating the
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 CC kinase having a hydrophobic pocket in the position equivalent to the
 CC hydrophobic pocket of human PDK1 that is defined by residues including
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
 CC PDK1 and further having a phosphate binding pocket in the position
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
 CC (M3) the activation state of a structure for a protein kinase; (3) a
 CC mutated protein kinase (1); (4) a polynucleotide (II) encoding (1); (5) a
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
 CC or (1) or an antibody reactive with PDK1 or (1) but not with the protein
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a

CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
 CC (1), (II) in medicine; (10) use of (V), (1), (II) for the manufacture of
 CC a medicament for the treatment of a patient in need of modulation of
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 CC p70 S6 kinase, for example insulin signalling pathway and/or
 CC PDK1/PKB/SGK/PRK2/p70 S6 kinase/PRK2/PRK2 signalling; and (11) a
 CC crystalline form (VI) of polypeptide as defined in (M1). (1) has
 CC antifungal, antidiabetic, cardiant, cytosolic, cerebroprotective,
 CC vasotropic and anorectic activities, and can be used as a modulator of
 CC protein kinase. (V) is useful for modulating the ability of protein
 CC kinase to phosphorylate different substrates, e.g., different naturally
 CC occurring polypeptides, to different extents. (V) inhibits or increases
 CC the activity of protein kinase. The protein structures e.g., the co-
 CC ordinates as provided in the specification are useful for designing
 CC reagent useful in drug designing assays or characterisation of protein
 CC kinase activity or regulation. (V) capable of producing the activity of
 CC PKC, e.g., PKC beta, PRK1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.
 XX

SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPGFSY 6
 |||||
 1 PPGFSY 6

Db 1 PPGFSY 6

RESULT 6
 ADS91353
 ID ADS91353 standard; peptide; 7 AA.
 XX
 AC ADS91353;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Protein kinase B alpha (PKBalpha) phosphorylated hydrophobic motif.
 XX
 KM AGC protein kinase; AGC protein kinase modulator; truncated AGC kinase;
 KM mutated AGC kinase; cytosolic; antinflammatory; antidiabetic;
 KM anorectic; abnormal cell proliferation; abnormal apoptosis; cancer;
 KM inflammation; diabetes; obesity; apoptosis inhibitor;
 KM protein kinase B alpha; PKBalpha; phosphorylated hydrophobic motif.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5 /note="phosphoserine"
 FT
 XX
 PN W02004035811-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 14-OCT-2003; 2003WO-GB004446.
 XX
 PR 14-OCT-2002; 2002GB-00023893.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Biondi RM, Frodin M, Antal TL;
 XX
 DR WPI; 2004-357223/33.
 XX
 PT Identifying AGC protein kinase modulators, for use in therapy, comprises

PT detecting the effect of a test agent on a polypeptide comprising a kinase
PT domain of an AGC protein kinase and associated activation loop.

PS Disclosure; Page 15; 65pp; English.

XX The present invention describes a method (M1) for identifying AGC protein
CC kinase (I) modulators, by: (a) providing a polypeptide comprising a
CC kinase domain of (I), and associated activation loop which may be
CC phosphorylated or unphosphorylated; (b) contacting a test agent (T) and
CC polypeptide(s) under conditions conducive to allow kinase activity to be
CC detected in absence of (T); and (c) detecting effect of (T) on kinase
CC activity. Also described: (1) a truncated AGC kinase polypeptide (II) for
CC use in (M1); (2) a mutated AGC kinase (III) comprising a mutation in a
CC kinase domain and/or activation loop in order to reduce binding ability
CC to the hydrophobic motif for use in (M1); (3) a compound/agent (IV)
CC identified by (M1) for use in therapy; (4) a phosphorylated peptide
CC comprising the sequence F/Y-X-X-F/Y-S/T-F in which the S/T residue is
CC phosphorylated; and (5) a peptide comprising the sequence F/Y-X-X-F/Y-E/D
CC -F. (I) has cytostatic, antiinflammatory, antidiabetic and anorectic
CC activities, and can be used as an AGC kinase activity modulator. The
CC method is useful for identifying agents which modulate AGC protein kinase
CC activity, such as an activator or inhibitor of AGC protein kinase
CC activity. (II) is useful in (M1). (III) is useful in (M1). (IV) is useful
CC for the manufacture of a medicament for use in therapy. (IV) is useful
CC for treating a subject who requires modulation of (I). (IV) is useful
CC inhibits AGC kinase activity is useful or treating diseases associated
CC with abnormal cell proliferation or apoptosis, such as cancer, or
CC undesirable inflammation. (IV) which activates or increases AGC kinase
CC activity is useful for treating diabetes or obesity, or is useful for
CC inhibiting apoptosis. The phosphorylated peptide is useful for modulating
CC AGC kinase activity. The unphosphorylated hydrophobic motif peptide, is
CC capable of inhibiting AGC kinase activity, and for designing new
CC inhibitory agents. The present sequence represents a protein kinase B
CC alpha (PKBalpha) phosphorylated hydrophobic motif, which is used in the
CC exemplification of the present invention.

XX Sequence 7 AA:

Query Match 100.0%; Score 35; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
| | | | |
Db 1 FPOFSY 6

RESULT 7
AAV93661

ID AAV93661 standard; peptide; 9 AA.

XX AAV93661;

DT 25-SEP-2000 (first entry)

DE PKB-alpha sequence for phosphorylation by protein kinase PDK2.

XX Protein kinase; Pkh1, Pkh2, Ypk1, Yrk2; protein kinase B-alpha;
KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
KM thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX Homo sapiens.

XX WO200036135-A2.

PD 22-JUN-2000.

PF 14-DEC-1999; 99WO-GB004228.

PR 14-DEC-1998; 98US-0112114P.

XX (MED1-) MEDICAL RES COUNCIL.

PA (REGC) UNIV CALIFORNIA.

XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;

DR WPI; 2000-442391/38.

PT Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer.

PS Disclosure; Fig 6A; 155pp; English.

XX The present sequence represents a sequence which is phosphorylated by
CC protein kinase PDK1. The specification describes a screening method to
CC identify a compound which modulates the activity of protein kinases from
CC different sources, using host yeast cells. The method is used to identify
CC a compound which modulates (inhibits) the activity of a protein kinase.
CC Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, human serum and
CC glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha
CC (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used
CC to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or
CC p70S6 kinase. Compounds identified by the methods are used to treat
CC fungal infections e.g. thrush, and to treat cancer. To treat cancer, the
CC compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds
CC which activate PKB or PDK1 can be used in the treatment of diabetes or
CC obesity, and compounds which inhibit a fungal functional homologue of
CC PDK1 (Pkh1 or Pkh2) or SGK (Ypk1 or Yrk2) can be used as an antifungal
CC agent to treat Candida infections, e.g. thrush.

XX Sequence 9 AA:

Query Match 100.0%; Score 35; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
| | | | |
Db 1 FPOFSY 6

RESULT 8
AAW51736

ID AAW51736 standard; peptide; 10 AA.

XX AAW51736;

DT 10-SEP-1998 (first entry)

DE Protein kinase RAC-PK/Akt alpha internal fragment.

XX Protein kinase; signalling pathway; antiproliferative; assay;
KW immunosuppressant agent; activation; mitogen; RSK; PKC-epsilon;
KW protein kinase C; RAC-PK.

XX Unidentified.

PN WO9818935-A2.

PD 07-MAY-1998.

PF 29-OCT-1997; 97WO-EP005979.

PR 31-OCT-1996; 96US-0030262P.

PA (NOVS) NOVARTIS AG.

XX Thomas G, Kozma S;

DR WPI; 1998-272228/24.

PT New protein kinase related to p70S6 pathway enzymes with threonine 389
PT replaced - by acidic amino acid, has constitutive activity, used to
PT identify potential antiproliferative and immunosuppressant agents, also
PT new dominant negative mutant of this enzyme.

CC acid sequence of a protein kinase ILK1 assay substrate from Akt3.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 35; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
DB 3 PPOFSY 8
RESULT 11
AAY94724
ID AAY94724 standard; peptide; 11 AA.
XX
AC AAY94724;
XX
DT 29-JAN-2001 (first entry)
XX
DE Antigenic peptide used to raise phospho-specific Ab against PKB.
XX
KM Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
KM protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
KM mechanical tissue damage; ischaemic disease; stroke;
KM myocardial infarction; antigenic peptide; protein kinase B.
XX
OS Unidentified.
XX
PN WO200056864-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB001004.
XX
PR 19-MAR-1999; 99GB-00006245.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Aleesi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
XX
DR WPI; 2000-647155/62.
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
PT interacting polypeptide.
XX
PS Example; Page 59; 103pp; English.
XX
CC This invention relates to a method for altering the substrate specificity
CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
CC an interacting polypeptide. Included in the invention are a preparation
CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
CC specificity is useful for phosphorylating a residue corresponding to the
CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
CC Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
CC protein kinase C related protein kinase 2 (PRK2). The compound identified
CC by methods of the invention that are capable of altering the substrate
CC specificity of PDK1 are useful for manufacturing a medicament for
CC treating a patient who is in need of modulation of the insulin signalling
CC pathway and/or PDK1, PDK2 or PRK2 signalling. A compound that is capable
CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1
CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
CC SGK, may be capable of providing a survival signal that protects cells
CC from apoptosis induced in a variety of ways. Reduction of the activity of
CC PDK1 may promote apoptosis and may be useful in treating cancer.
CC Conditions in which aiding apoptosis may be benefit may also include
CC resolution of inflammation. A compound capable of increasing the activity
CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
CC levels of leptin, which may lead to weight loss. The compounds may
CC suppress apoptosis, which may aid cell survival during or following cell

CC damaging processes and in treating disease in which apoptosis is
CC involved. Examples of the diseases include, mechanical (including heart)
CC tissue injury or ischemic disease, for example stroke and myocardial
CC infarction, or neural injury. The present sequence represents a peptide
CC used to raise phosph-specific antibodies against protein kinase B
CC phosphorylated at Ser 473. The peptide is used in methods to show that
CC PDK1 is responsible for the phosphorylation of PKB
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 35; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
DB 3 PPOFSY 8
RESULT 12
AAB59262
ID AAB59262 standard; peptide; 11 AA.
XX
AC AAB59262;
XX
DT 27-MAR-2001 (first entry)
XX
DE Phosphorylated peptide substrate #8.
XX
KM Phosphorylation; kinase; insulin.
XX
OS Unidentified.
XX
PN WO200075167-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US016025.
XX
PR 09-JUN-1999; 99US-0138311P.
XX
PR 10-JUN-1999; 99US-0138438P.
XX
PR 08-JUL-1999; 99US-00349733.
XX
PR 28-APR-2000; 2000US-0200594P.
XX
PA (LJLB-) LJL BIOSYSTEMS INC.
XX
PI Sportsman JR, Hoekstra ME, Lee SK, Cairns N, Kauvar LM;
XX
DR WPI; 2001-091201/10.
XX
PT Assay for detecting phosphorylation and dephosphorylation modification of
PT proteins by contacting luminescence peptide with a binding partner and
PT measuring change in luminescence polarization.
XX
PS Claim 13; Page 57; 89pp; English.
XX
CC The present invention relates to detecting addition or removal of a
CC phosphate group to or from a substrate. The method involves contacting a
CC luminescent peptide with a binding partner that binds specifically to a
CC phosphorylated peptide without regard to the particular amino acid
CC sequence of the peptide. The method is useful for detecting
CC phosphorylation and dephosphorylation modifications of proteins,
CC including kinases and phosphatases. The methods can be used to study the
CC kinase activity of different receptors e.g. the insulin receptor and to
CC find agonists and antagonists of these receptors
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 35; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6

Db 3 FPOFSY 8

RESULT 13
ADRO6310
ID ADRO6310 standard; peptide; 11 AA.
AC ADRO6310;
XX
XX

DT 07-OCT-2004 (first entry)

DE Protein kinase B/ Akt switch control ligand, SEQ ID 8.

XX Switch control ligand; switch control pocket;

KM protein activity modulation; human; Akt1; protein kinase B.

XX Homo sapiens.

OS Key Location/Qualifiers
FH Modified-site 7

FT /note= "This residue becomes phosphorylated upon
FT activation by upstream kinase regulatory kinases"

XX WO2004061084-A2.

XX 22-JUL-2004.

PF 26-DEC-2003; 2003WO-US041450.

XX 31-DEC-2002; 2002US-0437304P.

PR 31-DEC-2002; 2002US-0437403P.

PR 31-DEC-2002; 2002US-0437415P.

PR 31-DEC-2002; 2002US-0437487P.

PR 18-APR-2003; 2003US-0463804P.

PR 24-DEC-2003; 53US-00463804.

XX (DECI-) DECIPHERA PHARM INC.

PA Flynn DL, Petrillo PA;

XX WPI; 2004-534376/51.

XX Identifying molecules that interact with specific naturally occurring
PT proteins for modulating protein activity, comprises identifying molecules
PT that bind with the protein at the region of the pocket to regulate
PT activity of the protein.

PS Disclosure, SEQ ID NO 8; 204pp; English.

XX The present invention relates to a method for identifying molecules,
CC which interact with proteins e.g. enzymes, receptors, or signaling
CC proteins, in order to regulate the activity of the proteins. The method
CC comprises: identifying a switch control ligand forming a part of the
CC protein; identifying a switch control pocket forming a part of the
CC protein; and which interacts with the switch control ligand, where the
CC ligand interacting in vivo with the pocket to regulate the conformation
CC and biological activity of the protein so that the protein will assume a
CC first conformation and a first biological activity upon the ligand-pocket
CC interaction, and will assume a second, different conformation and a
CC biological activity in the absence of the ligand-pocket interaction;
CC providing respective samples of the protein in the first and second
CC conformations; and screening at least one of the samples against one or
CC more candidate molecules by contacting the molecules and one sample, and
CC identifying small molecules which bind with the protein at the region of
CC the pocket in order to regulate the activity of the protein. The method
CC is useful for modulating protein activity and for the identification of
CC new pharmacological compounds and for treatment modalities. The present
CC sequence is one such switch control ligand, which is specific to protein
CC kinase B/ Akt.
XX
XX Sequence 11 AA;

Query Match 100.0%; Score 35; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 3 FPOFSY 8

RESULT 14
AAW34387
ID AAW34387 standard; peptide; 12 AA.
XX
XX

AC AAW34387;

DT 04-MAR-1998 (first entry)

DE PKB C-terminal fragment.

XX Protein kinase B; PKB; substrate; glycogen metabolism; pancreatic cancer;

KM regulator; protein synthesis; enzyme modulator; type II diabetes;

KW insulin-stimulated crosside kinase; breast cancer; ovarian cancer;

KM therapy; RAC; protooncogene Akt.

XX Homo sapiens.

XX WO9722360-A2.

XX 26-JUN-1997.

PF 20-DEC-1996; 96WO-GB003186.

XX 20-DEC-1995; 95GB-00026083.

PR 16-MAY-1996; 96GB-00010272.

PR 18-JUL-1996; 96GB-00015066.

XX (MEDI-) MEDICAL RES COUNCIL.

PA (UYDU-) UNIT DUNDEE.

XX Cohen P, Alessi D, Cross D;

XX WPI; 1997-341435/31.

XX Use of protein kinase B for regulation of glycogen metabolism and protein
PT synthesis - also peptide substrates for PKB and methods for screening for
PT modulators.

PS Example 1; Page 11; 98pp; English.

XX This sequence represents a C-terminal fragment of protein kinase B (PKB).
CC PKB is also known as the protooncogene Akt, and RAC. This sequence was
CC used as an epitope to produce PKB specific antibodies. The use of PKB,
CC its analogues, isoforms, inhibitors, activators and/or functional
CC equivalents for regulating glycogen metabolism and/or protein synthesis
CC is the subject of the invention. This sequence can also be used in a
CC method of the invention for identifying agents that modulate the activity
CC of PKB. It can also be used to screen for modulators of enzymes that
CC catalyse PKB phosphorylation. PKB (an insulin-stimulated crosside
CC kinase) and its analogues etc. are used to treat disease characterized by
CC abnormal glycogen metabolism and/or protein synthesis, especially type II
CC diabetes and cancer (specifically of breast, pancreas and ovary). The
CC various screening methods are used to identify agents potentially useful
CC for treating these diseases
XX

SO Sequence 12 AA;

Query Match 100.0%; Score 35; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 1 FPOFSY 6

RESULT 15

ABO19480

ID ABO19480 standard; peptide; 12 AA.

XX

AC ABO19480;

XX

DT 27-AUG-2003 (first entry)

XX

DE C-terminus region of protein kinase Akt.

XX

KM Protein kinase; kinase; enzyme; rational drug design; non-crystallisable;

XX

KM sulindac sulphide; PD98059.

XX

OS Unidentified.

XX

PN US2003032649-A1.

XX

PD 13-FEB-2003.

XX

PF 31-JUL-2001; 2001US-00918873.

XX

PR 31-JUL-2001; 2001US-00918873.

XX

PA (GOLD/) GOLDSMITH E J.

XX

PA (RADH/) RADHA A.

XX

PA (GAYN/) GAYNOR R B.

XX

PI Goldsmith EJ, Radha A, Gaynor RB;

XX

DR WPI; 2003-492076/46.

XX

PT Novel chimeric protein kinase for identifying inhibitor molecules, has

XX

PT inhibitor binding site of first protein kinase which bind to inhibitor

XX

PT and amino acids of second protein kinase which do not bind to inhibitor.

XX

PS Disclosure; Fig 7; 21pp; English.

XX

CC The invention relates to a chimeric protein kinase having an inhibitor

CC

CC binding site comprising amino acid residues of a first protein kinase

CC

CC which bind an inhibitor and residues of a second protein kinase which do

CC

CC not bind the inhibitor. The chimeric protein kinase is useful for

CC

CC identifying inhibitor molecules capable of affecting the activity of

CC

CC first protein kinase, by preparing the chimeric protein kinase, growing a

CC

CC crystal of the chimeric protein kinase, solving the structure of crystal

CC

CC of chimeric protein kinase, using X-ray crystallography methods and using

CC

CC the structure to design inhibitor molecules capable of affecting the

CC

CC activity of the first protein kinase. The structure of the chimeric

CC

CC protein kinase is useful for the rational drug design of inhibitors of

CC

CC non-crystallisable protein kinase. The present sequence represents the

CC

CC amino acid sequence of a protein kinase region near the binding site for

CC

CC sulindac sulphide and PD98059

XX

SQ Sequence 12 AA;

XX

Query March

Best Local Similarity 100.0%; Score 35; DB 6; Length 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPQFSY 6

Db 7 FPQFSY 12

Search completed: June 14, 2006, 02:09:02
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OM protein - protein search, using sw model

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Perfect score: 35
Sequence: 1 fpgfsy 6

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5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCFUS.COMB.pep:*
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7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	352	2	US-09-771-161A-157
2	35	100.0	417	2	US-09-590-740-4
3	35	100.0	479	2	US-09-771-161A-246
4	35	100.0	479	2	US-09-771-161A-247
5	35	100.0	479	2	US-09-771-161A-248
6	35	100.0	480	2	US-09-091-058-2
7	35	100.0	480	2	US-09-590-740-2
8	35	100.0	480	2	US-09-590-740-6
9	35	100.0	480	2	US-09-538-092-1053
10	35	100.0	480	2	US-09-205-658-157
11	35	100.0	480	2	US-09-526-043-13
12	35	100.0	480	2	US-09-526-043-14
13	35	100.0	480	2	US-09-771-161A-223
14	35	100.0	481	2	US-09-538-092-1054
15	35	100.0	726	2	US-09-417-197-71
16	35	100.0	727	2	US-09-417-197-119
17	32	91.4	401	2	US-09-248-796A-17808
18	30	85.7	112	2	US-09-621-976-5729
19	30	85.7	152	2	US-09-621-976-4568
20	30	85.7	218	2	US-09-270-767-60058
21	30	85.7	449	2	US-10-094-749-2893
22	30	85.7	606	2	US-10-094-749-2892
23	30	85.7	733	2	US-09-328-352-6242
24	30	85.7	788	2	US-09-270-767-44611
25	30	85.7	858	2	US-09-538-092-674
26	29	82.9	59	2	US-09-270-767-40021

27	29	82.9	59	2	US-09-270-767-55237	Sequence 55237, A
28	29	82.9	90	2	US-09-270-767-36421	Sequence 36421, A
29	29	82.9	90	2	US-09-270-767-51638	Sequence 51638, A
30	29	82.9	129	2	US-09-270-767-33659	Sequence 33659, A
31	29	82.9	129	2	US-09-270-767-48876	Sequence 48876, A
32	29	82.9	231	2	US-09-896-522-4	Sequence 4, Appl1
33	29	82.9	320	2	US-09-107-532A-4408	Sequence 4408, Ap
34	29	82.9	320	2	US-09-270-767-42941	Sequence 42941, A
35	29	82.9	395	2	US-09-248-796A-16028	Sequence 16028, A
36	29	82.9	521	2	US-10-155-535-6	Sequence 6, Appl1
37	29	82.9	640	2	US-09-177-165A-30	Sequence 30, Appl1
38	29	82.9	651	2	US-09-248-796A-20333	Sequence 20333, A
39	29	82.9	678	2	US-09-487-558B-314	Sequence 314, App
40	29	82.9	686	2	US-09-134-000C-5066	Sequence 5066, Ap
41	29	82.9	1003	1	US-07-991-867B-6	Sequence 6, Appl1
42	29	82.9	1003	1	US-08-107-755A-6	Sequence 6, Appl1
43	29	82.9	1003	1	US-08-544-332-6	Sequence 6, Appl1
44	29	82.9	1003	2	US-09-370-861A-6	Sequence 6, Appl1
45	29	82.9	1134	2	US-10-154-419-34	Sequence 34, Appl1

ALIGNMENTS

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RESULT 1
US-09-771-161A-157
; Sequence 157, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724.676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 157
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-157

Query Match      100.0%; Score 35; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. NO. 24;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  PPGFSY 6
Db      341 PPGFSY 346

RESULT 2
US-09-590-740-4
; Sequence 4, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590.740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 417
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-590-740-4

Query Match 100.0%; Score 35; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 406 FPOFSY 411

RESULT 3
US-09-771-161A-246
Sequence 246, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 246
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match 100.0%; Score 35; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 468 FPOFSY 473

RESULT 4
US-09-771-161A-247
Sequence 247, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 247
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match 100.0%; Score 35; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 468 FPOFSY 473

RESULT 5
US-09-771-161A-248
Sequence 248, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 248
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match 100.0%; Score 35; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 468 FPOFSY 473

RESULT 6
US-09-091-058-2
Sequence 2, Application US/09091058
Patent No. 6054285
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A.
APPLICANT: Frech, Matthias
TITLE OF INVENTION: Screening Method
FILE REFERENCE: 4-20683/A/20684/PCT
CURRENT APPLICATION NUMBER: US/09/091,058
CURRENT FILING DATE: 1998-06-10
EARLIER APPLICATION NUMBER: PCT/EP96/04814
EARLIER FILING DATE: 1996-11-05
EARLIER APPLICATION NUMBER: 9525703.6
EARLIER FILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
US-09-091-058-2

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 469 FPOFSY 474

RESULT 7
US-09-590-740-2

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; Sequence 2, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-740-2

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 8
US-09-590-740-6
; Sequence 6, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-590-740-6

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 9
US-09-538-092-1053
; Sequence 1053, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Manfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
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; SEQ ID NO 1053
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P1749
US-09-538-092-1053

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 10
US-09-205-658-157
; Sequence 157, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-658-157

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 11
US-09-526-043-13
; Sequence 13, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 480
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-526-043-13

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 470 FPOFSY 475

RESULT 12
US-09-526-043-14
Sequence 14, Application US/09526043
Patent No. 6881555
GENERAL INFORMATION:
APPLICANT: Guo, Kun
APPLICANT: Pagnoni, Marco
APPLICANT: Clark, Kenneth
APPLICANT: Ivashchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/09/526,043
CURRENT FILING DATE: 2000-03-14
EARLIER APPLICATION NUMBER: 60/125,108
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
US-09-526-043-14

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 13
US-09-771-161A-223
Sequence 223, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 223
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-223

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 14
US-09-538-092-1054
Sequence 1054, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratPatSegFormatter Version 0.9
SEQ ID NO 1054
LENGTH: 481
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P31751
US-09-538-092-1054

Query Match 100.0%; Score 35; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 470 FPOFSY 475

RESULT 15
US-09-417-197-71
Sequence 71, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Ir
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 71
LENGTH: 726
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PKB-EGFP fusion
US-09-417-197-71

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Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

Search completed: June 14, 2006, 02:18:40

Wed Jun 14 13:58:13 2006

Job time : 39 secs

09937009-b.ral

Page 5

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:29 ; Search time 124.5 Seconds

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Title: 09937009-B

Perfect score: 35

Sequence: 1 fpgfsy 6

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Post-processing: Minimum Match 0%

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	US-10-014-485A-145	Sequence 145, App
2	35	100.0	6	US-10-148-786A-46	Sequence 46, Appl
3	35	100.0	6	US-10-217-574-6	Sequence 6, Appl
4	35	100.0	6	US-10-217-555-5	Sequence 5, Appl
5	35	100.0	6	US-10-217-555-12	Sequence 12, Appl
6	35	100.0	7	US-09-845-667-12	Sequence 12, Appl
7	35	100.0	10	US-10-317-550-8	Sequence 8, Appl
8	35	100.0	10	US-10-317-550-9	Sequence 9, Appl
9	35	100.0	11	US-10-746-545-8	Sequence 8, Appl
10	35	100.0	12	US-09-845-667-3	Sequence 3, Appl
11	35	100.0	12	US-09-918-873-24	Sequence 24, Appl
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14	35	100.0	13	US-10-823-433-24	Sequence 24, Appl
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16	35	100.0	15	US-10-823-433-22	Sequence 22, Appl
17	35	100.0	16	US-10-517-904-1	Sequence 1, Appl
18	35	100.0	20	US-10-485-788A-622	Sequence 622, App
19	35	100.0	22	US-10-217-574-22	Sequence 22, Appl
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21	35	100.0	335	US-10-746-545-24	Sequence 24, Appl
22	35	100.0	335	US-10-746-545-37	Sequence 37, Appl
23	35	100.0	336	US-10-217-574-21	Sequence 21, Appl
24	35	100.0	336	US-10-217-555-21	Sequence 21, Appl
25	35	100.0	332	US-09-771-161A-157	Sequence 157, App
26	35	100.0	417	US-10-713-678-4	Sequence 4, Appl
27	35	100.0	479	US-09-771-161A-246	Sequence 246, App

28	35	100.0	479	3	US-09-771-161A-247	Sequence 247, App
29	35	100.0	479	3	US-09-771-161A-248	Sequence 248, App
30	35	100.0	479	3	US-10-394-322A-3	Sequence 3, Appl
31	35	100.0	479	4	US-10-217-574-33	Sequence 33, Appl
32	35	100.0	479	4	US-10-217-555-33	Sequence 33, Appl
33	35	100.0	479	5	US-10-753-267-108	Sequence 108, App
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37	35	100.0	480	3	US-09-526-043-13	Sequence 13, Appl
38	35	100.0	480	3	US-09-526-043-14	Sequence 14, Appl
39	35	100.0	480	3	US-09-963-693-157	Sequence 157, App
40	35	100.0	480	4	US-10-060-065-18	Sequence 18, Appl
41	35	100.0	480	4	US-10-059-585-39	Sequence 39, Appl
42	35	100.0	480	4	US-10-394-322A-1	Sequence 1, Appl
43	35	100.0	480	4	US-10-394-568-11	Sequence 11, Appl
44	35	100.0	480	4	US-10-217-574-31	Sequence 31, Appl
45	35	100.0	480	4	US-10-217-555-31	Sequence 31, Appl

ALIGNMENTS

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RESULT 1
US-10-014-485A-145
; Sequence 145, Application US/10014485A
; Publication No. US20020168684A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES US
; FILE REFERENCE: CST-138 CIP2
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US/10/014,485A
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)-(5)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated
US-10-014-485A-145
Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 PPGFSY 6
Db 1 PPGFSY 6
RESULT 2
US-10-148-786A-46
; Sequence 46, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
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; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-786A-46

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```

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PPOFSY 6
        |||||
Db      1 PPOFSY 6

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RESULT 3
US-10-217-574-6
; Sequence 6, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-574-6

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Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PPOFSY 6
        |||||
Db      1 PPOFSY 6

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RESULT 4
US-10-217-555-5
; Sequence 5, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentln Ver. 2.1

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; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-5

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```

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PPOFSY 6
        |||||
Db      1 PPOFSY 6

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```

RESULT 5
US-10-217-555-12
; Sequence 12, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-12

```

```

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 PPOFSY 6
        |||||
Db      1 PPOFSY 6

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RESULT 6
US-09-845-667-12
; Sequence 12, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; APPLICANT: Alessi, David
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Braham & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-845-667-12

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
|||
Db 2 PPOFSY 7

RESULT 7
US-10-317-550-8
Sequence 8, Application US/10317550
Publication No. US20030166034A1
GENERAL INFORMATION:
APPLICANT: Thomas, George
APPLICANT: Kozma, Sara
TITLE OF INVENTION: P70-S6K or Related Kinase With
FILE REFERENCE: 4-20793/A/PCT
CURRENT APPLICATION NUMBER: US/10/317,550
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: US/09/297,404B
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-317-550-8

Query Match 100.0%; Score 35; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
|||
Db 2 PPOFSY 7

RESULT 8
US-10-317-550-9

Sequence 9, Application US/10317550
Publication No. US20030166034A1
GENERAL INFORMATION:
APPLICANT: Thomas, George
APPLICANT: Kozma, Sara
TITLE OF INVENTION: P70-S6K or Related Kinase With
FILE REFERENCE: 4-20793/A/PCT
CURRENT APPLICATION NUMBER: US/10/317,550
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: US/09/297,404B
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-317-550-9

Query Match 100.0%; Score 35; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
|||
Db 2 PPOFSY 7

RESULT 9
US-10-746-545-8
Sequence 8, Application US/10746545
Publication No. US20040171075A1
GENERAL INFORMATION:
APPLICANT: Deciphra Pharmaceuticals, Inc.
APPLICANT: Flynn, Daniel L
APPLICANT: Pecilio, Peter A
TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
FILE REFERENCE: 34475
CURRENT APPLICATION NUMBER: US/10/746,545
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: US 60/437,487
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-746-545-8

Query Match 100.0%; Score 35; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
|||
Db 3 PPOFSY 8

RESULT 10
US-09-845-667-3
Sequence 3, Application US/09845667
Patent No. US20020065221A1
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
APPLICANT: Alessi, Dario
APPLICANT: Cross, Darren

TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Braman & Rogalskyj, LLP
STREET: P.O. Box 352

```

; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-845-667-3
;
Query Match      100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPOFSY 6
Db      1 PPOFSY 6

RESULT 11
US-09-918-873-24
; Sequence 24, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radha, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; DATABASE ACCESSION NUMBER: P4197
; DATABASE ENTRY DATE: 1996-06-01
US-09-918-873-24
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Query Match      100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPOFSY 6
Db      7 PPOFSY 12

RESULT 12
US-10-823-433-7
; Sequence 7, Application US/10823433
; Publication No. US20050053594A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian Arthur
; APPLICANT: Andjelkovic, Mirjana
; APPLICANT: Cron-Holman, Peter
; APPLICANT: Cohen, Philip
; APPLICANT: Alesai, Darlo
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: RAC-PK AS A THERAPEUTIC AGENT OR IN
; TITLE OF INVENTION: DIAGNOSTICS, SCREENING METHOD FOR AGENTS AND PROCESS FOR
; FILE REFERENCE: 4-20635B/4-20682C/4-3718B/N1
; CURRENT APPLICATION NUMBER: US/10/823,433
; CURRENT FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2002-05-16
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 2001-10-03
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 2001-04-30
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (469)...(480)
; OTHER INFORMATION: C-Terminal peptide of Human RAC-PK
US-10-823-433-7

Query Match      100.0%; Score 35; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PPOFSY 6
Db      1 PPOFSY 6

RESULT 13
US-09-845-667-31
; Sequence 31, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
```

APPLICANT: Cohen, Philip
Aleesi, Darlen
Cross, Darren
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brame & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STATE: New York
COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brame, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-845-667-31
Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
Db 5 PPOFSY 10
RESULT 14
US-10-823-433-24
Sequence 24, Application US/10823433
Publication No. US20050053594A1
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian Arthur
APPLICANT: Andjelkovic, Mirjana
APPLICANT: Ciron-Hofman, Peter
APPLICANT: Cohen, Philip
APPLICANT: Aleesi, Darlen
APPLICANT: Cross, Darren
TITLE OF INVENTION: RAC-PK AS A THERAPEUTIC AGENT OR IN
DIAGNOSTICS, SCREENING METHOD FOR AGENTS AND PROCESS FOR
TITLE OF INVENTION: ACTIVATING RAC-PK

FILE REFERENCE: 4-20635B/4-20682C/4-33718B/N1
CURRENT APPLICATION NUMBER: US/10/823,433
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 10/147,123
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/542,646
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 09/091,109
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: PCT/EP96/04811
PRIOR FILING DATE: 1996-11-05
PRIOR APPLICATION NUMBER: 09/970,000
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 09/068,702
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: PCT/EP96/04810
PRIOR FILING DATE: 1996-11-05
PRIOR APPLICATION NUMBER: 10/673,091
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/845,667
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/091,763
PRIOR FILING DATE: 1998-06-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-823-433-24
Query Match 100.0%; Score 35; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
Db 5 PPOFSY 10
RESULT 15
US-09-845-667-29
Sequence 29, Application US/09845667
Patent No. US20020065221A1
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
Aleesi, Darlen
Cross, Darren
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brame & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STATE: New York
COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998

APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-845-667-29

Query Match 100.0%; Score 35; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPOFSY 6
Db 4 FPOFSY 9

Search completed: June 14, 2006, 02:37:58
Job time : 125.5 secs